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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

FIRST-NAMED INVENTOR OR
APPLICATION IDENTIFIER: Richard A. Shimkets

FOR: **NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE
POLYMORPHISMS AND METHODS OF USE THEREOF**

November 22, 2000
Boston, Massachusetts

Box PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

**REQUEST FOR FILING A NEW NONPROVISIONAL APPLICATION
UNDER 37 C.F.R. §1.53(b)**

1. This is a request for filing a new nonprovisional application under 37 C.F.R. §1.53(b).
2. ☒ Specification and Drawings (Total pages: 682);
Specification (50 pages); Claims (10 pages); Abstract (1 page); Sequence Listing
(431 pages); and Table 1 (190 pages).
3. ☒ Declaration and Power of Attorney
☒ Unsigned
☐ Signed
4. ☐ Information Disclosure Statement (IDS)
☐ Copy of IDS and PTO-1449 (___ pages)
☐ Copies of references cited
5. ☐ Assignment Papers
☐ Recordation Form Cover Sheet (PTO-1595)
☐ Assignment Document
6. ☐ Statement Claiming Small Entity Status
☐ Claiming Small Entity As Independent Inventor (37 C.F.R. §§1.9(f) & 1.27(b)).
☐ Claiming Small Entity As Small Business Concern (37 C.F.R. §§1.9(f) & 1.27(c)).
☐ Claiming Small Entity As Nonprofit Organization (37 C.F.R. §§1.9(f) & 1.27(d)).

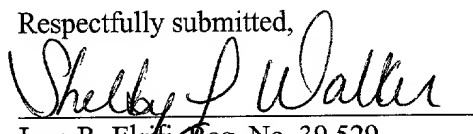
FIRST-NAMED INVENTOR OR **Richard A. Shimkets**
APPLICATION IDENTIFIER:
Request for New Nonprovisional Application (37 C.F.R. §1.53(b))

7. Fee Calculation

| CLAIMS AS FILED | | | | | |
|--|-----------------|------------------------|-----------------|--|---|
| Claims | Number Filed | Basic Fee Allowance | Number Extra | Rate | Basic Fee 37 C.F.R. 1.16(a) \$ 710.00 |
| Total Claims (37 C.F.R. 1.16(c)) | 44 | - 20 = | 24 | \$ 18.00 | \$ 432.00 |
| Independent Claims (37 C.F.R. 1.16(b)) | 11 | - 3 = | 8 | \$ 80.00 | \$ 640.00 |
| Multiple Dependent Claim(s), if any (37 C.F.R. 1.16(d)) | | | | \$260.00 | 0 |
| | | | | SUBTOTAL: | \$1,782.00 |
| | | | | Reduction by 50% for filing by small entity: | 891.00 |
| | | | | TOTAL FEE: | \$891.00 |

8. ☒ A check in the amount of **\$891.00** is enclosed.
9. ☒ The Commissioner is hereby authorized to credit overpayments or charge the following fees to Deposit Account No. 50-0311, Ref. No. 15966-565 (CURA-65):
- ☒ Fees required under 37 C.F.R. §1.16;
- ☒ Fees required under 37 C.F.R. §1.17;
- ☒ Fees required under 37 C.F.R. §1.18.
10. ☒ Return Receipt Postcard Enclosed.
11. ☐ Other Documents Enclosed:
- ☐ Change of Attorney Address In Application.
- ☐ Limited Recognition under 37 C.F. § 10.9(b) for Michel Morency.

Respectfully submitted,



Dated: November 22, 2000

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TRADOCS:1403439 1(%2WF011.DOC)

NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

RELATED APPLICATIONS

This application claims priority to U.S.S.N. 60/167,383, filed November 24, 1999, which is incorporated herein by reference in its entirety.

BACKGROUND OF THE INVENTION

Sequence polymorphism-based analysis of nucleic acid sequences can augment or replace previously known methods for determining the identity and relatedness of individuals. The approach is generally based on alterations in nucleic acid sequences between related individuals. This analysis has been widely used in a variety of genetic, diagnostic, and forensic applications. For example, polymorphism analyses are used in identity and paternity analysis, and in genetic mapping studies.

One such type of variation is a restriction fragment length polymorphism (RFLP). RFLPS can create or delete a recognition sequence for a restriction endonuclease in one nucleic acid relative to a second nucleic acid. The result of the variation is an alteration in the relative length of restriction enzyme generated DNA fragments in the two nucleic acids.

Other polymorphisms take the form of short tandem repeats (STR) sequences, which are also referred to as variable numbers of tandem repeat (VNTR) sequences. STR sequences typically that include tandem repeats of 2, 3, or 4 nucleotide sequences that are present in a nucleic acid from one individual but absent from a second, related individual at the corresponding genomic location.

Other polymorphisms take the form of single nucleotide variations, termed single nucleotide polymorphisms (SNPs), between individuals. A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP

originates as a cDNA.

SNPs can arise in several ways. A single nucleotide polymorphism may arise due to a substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the replacement of one purine nucleotide by another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or the converse.

Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Thus, the polymorphic site is a site at which one allele bears a gap with respect to a single nucleotide in another allele.

Some SNPs occur within, or near genes. One such class includes SNPs falling within regions of genes encoding for a polypeptide product. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product and give rise to the expression of a defective or other variant protein. Such variant products can, in some cases result in a pathological condition, *e.g.*, genetic disease. Examples of genes in which a polymorphism within a coding sequence gives rise to genetic disease include sickle cell anemia and cystic fibrosis. Other SNPs do not result in alteration of the polypeptide product. Of course, SNPs can also occur in noncoding regions of genes.

SNPs tend to occur with great frequency and are spaced uniformly throughout the genome. The frequency and uniformity of SNPs means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest.

SUMMARY OF THE INVENTION

The invention is based in part on the discovery of novel single nucleotide polymorphisms (SNPs) in regions of human DNA.

Accordingly, in one aspect, the invention provides an isolated polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 1468) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it

includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS: 1-1468), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

5 The polynucleotide can be, *e.g.*, DNA or RNA, and can be between about 10 and about 100 nucleotides, *e.g.* 10-90, 10-75, 10-51, 10-40, or 10-30, nucleotides in length.

 In some embodiments, the polymorphic site in the polymorphic sequence includes a nucleotide other than the nucleotide listed in Table 1, column 5 for the polymorphic sequence, *e.g.*, the polymorphic site includes the nucleotide listed in Table 1, column 6
10 for the polymorphic sequence.

 In other embodiments, the complement of the polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of the polymorphic sequence, *e.g.*, the complement of the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

15 In some embodiments, the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to an ATPase associated protein, a cadherin, or any of the other proteins identified in Table 1, column 10.

 In another aspect, the invention provides an isolated allele-specific
20 oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide
25 sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the complementary nucleotide

sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

5 In some embodiments, the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide. The second polynucleotide can be, *e.g.*, (a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), wherein the polymorphic sequence includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence; (b) a nucleotide sequence that is a fragment of
10 any of the polymorphic sequences; (c) a complementary nucleotide sequence including a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), wherein the polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and (d) a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the
15 polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The invention also provides a method of detecting a polymorphic site in a nucleic
20 acid. The method includes contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the
25 nucleotide recited in Table 1, column 5. The method also includes determining whether the nucleic acid and the oligonucleotide hybridize. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphic site in the nucleic acid.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

In some embodiments, the polymorphic sequence identified by the oligonucleotide is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated polypeptide related to an ATPase associated protein, cadherin, or any of the other protein families identified in Table 1, column 10.

In another aspect, the method includes determining if a sequence polymorphism is the present in a subject, such as a human. The method includes providing a nucleic acid from the subject and contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. Hybridization between the nucleic acid and the oligonucleotide is then determined. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphism in said subject.

In a further aspect, the invention provides a method of determining the relatedness of a first and second nucleic acid. The method includes providing a first nucleic acid and a second nucleic acid and contacting the first nucleic acid and the second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1,

column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the first nucleic acid and the second nucleic acid hybridize to the oligonucleotide, and comparing hybridization of the first and second nucleic acids to the oligonucleotide. Hybridization of first and second nucleic acids to the nucleic acid indicates the first and second subjects are related.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The method can be used in a variety of applications. For example, the first nucleic acid may be isolated from physical evidence gathered at a crime scene, and the second nucleic acid may be obtained from a person suspected of having committed the crime. Matching the two nucleic acids using the method can establish whether the physical evidence originated from the person.

In another example, the first sample may be from a human male suspected of being the father of a child and the second sample may be from the child. Establishing a match using the described method can establish whether the male is the father of the child.

In another aspect, the invention provides an isolated polypeptide comprising a polymorphic site at one or more amino acid residues, and wherein the protein is encoded by a polynucleotide including one of the polymorphic sequences SEQ ID NOS:1-1468, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the

complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

The polypeptide can be, *e.g.*, related to one of the protein families disclosed herein. For example, polypeptide can be related to an ATPase associated protein, cadherin, or any of the other proteins provided in Table 1, column 10.

In some embodiments, the polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

In some embodiments, the polypeptide encoded by the polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

The invention also provides an antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-1468, or its complement. The polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

In some embodiments, the antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

Preferably, the antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

The invention further provides a method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject. The

method includes providing a protein sample from the subject and contacting the sample with the above-described antibody under conditions that allow for the formation of antibody-antigen complexes. The antibody-antigen complexes are then detected. The presence of the complexes indicates the presence of the polypeptide.

5 The invention also provides a method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, *e.g.*, a human, non-human primate, cat, dog, rat, mouse, cow, pig, goat, or rabbit. The method includes providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic
10 sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or its complement, and treating the subject by administering to the subject an effective dose of a therapeutic agent. Aberrant expression can include qualitative alterations in expression of a gene, *e.g.*, expression of a gene encoding a polypeptide having an altered amino acid sequence with respect to its wild-type counterpart. Qualitatively different polypeptides
15 can include, shorter, longer, or altered polypeptides relative to the amino acid sequence of the wild-type polypeptide. Aberrant expression can also include quantitative alterations in expression of a gene. Examples of quantitative alterations in gene expression include lower or higher levels of expression of the gene relative to its wild-type counterpart, or alterations in the temporal or tissue-specific expression pattern of a gene. Finally,
20 aberrant expression may also include a combination of qualitative and quantitative alterations in gene expression.

 The therapeutic agent can include, *e.g.*, second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele. In some embodiments, the second nucleic acid sequence
25 comprises a polymorphic sequence which includes nucleotide listed in Table 1, column 5 for the polymorphic sequence.

 Alternatively, the therapeutic agent can be a polypeptide encoded by a polynucleotide comprising polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is

complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

The therapeutic agent may further include an antibody as herein described, or an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for the polymorphic sequence.

In another aspect, the invention provides an oligonucleotide array comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468); a nucleotide sequence that is a fragment of any of the nucleotide sequences, provided that the fragment includes a polymorphic site in the polymorphic sequence; a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468); or a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In preferred embodiments, the array comprises 10; 100; 1,000; 10,000; 100,000 or more oligonucleotides.

The invention also provides a kit comprising one or more of the herein-described nucleic acids. The kit can include, *e.g.*, a polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 1468) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS:1-1468), or a

fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence. The invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides human SNPs in sequences which are transcribed, *i.e.*, are cSNPs. As is explained in more detail below, many SNPs have been identified in genes related to polypeptides of known function. For some applications, SNPs associated with various polypeptides can be used together. For example, SNPs can be group according to whether they are derived from a nucleic acid encoding a polypeptide related to a particular protein family or involved in a particular function. Thus, SNPs related to ATPase associated protein may be collected for some applications, as may SNPs associated with cadherin, or ephrin (EPH), or any of the other proteins recited in Table 1, column 10. Similarly, SNPs can be grouped according to the functions played by their gene products. Such functions include, e.g., structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism.

The SNPs are shown in Table 1 and the Sequence Listing. Both provide a summary of the polymorphic sequences disclosed herein. In the Table, a “SNP” is a polymorphic site embedded in a polymorphic sequence. The polymorphic site is occupied by a single nucleotide, which is the position of nucleotide variation between the wild type and polymorphic allelic sequences. The site is usually preceded by and followed by relatively highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations). Thus, a polymorphic sequence can include one or more of the following sequences: (1) a sequence having the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence; or (2) a sequence having a nucleotide other than the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence. An example of the latter sequence is a polymorphic sequence having the nucleotide denoted in Table 1, column 6 at the polymorphic site in the polymorphic sequence.

Nucleotide sequences for a referenced-polymorphic pair are presented in Table 1. Each cSNP entry provides information concerning the wild type nucleotide sequence as well as the corresponding sequence that includes the SNP at the polymorphic site. Since

the wild type sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele; its SEQ ID NO: is also cross referenced in the Table 1. A reference to the SEQ ID NO: giving the translated amino acid sequence is also given if appropriate. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and an explanation for each, are given below.

“SEQ ID” provides the cross-reference to the nucleotide SEQ ID NO:, and, as explained below, an amino acid SEQ ID NO: as well, in the Sequence Listing of the application. Conversely, each sequence entry in the Sequence Listing also includes a cross-reference to the CuraGen sequence ID, under the label “CuraGen Sequence ID”. The first SEQ ID NO: given in the first column of each row of the Table is the SEQ ID NO: identifying the nucleic acid sequence for the polymorphism. If a polymorphism carries an entry for the amino acid portion of the row, a second SEQ ID NO: appears in parentheses in the column “Amino acid after” (see below). This second SEQ ID NO: refers to an amino acid sequence giving the polymorphic amino acid sequence that is the translation of the nucleotide polymorphism. If a polymorphism carries no entry for the protein portion of the row, only one SEQ ID NO: is provided.

“CuraGen sequence ID” provides CuraGen Corporation’s accession number.

“Base pos. of SNP” gives the numerical position of the nucleotide in the reference, or wild-type, gene at which the cSNP is found. This enumeration of bases is that found in the public database from which the reference gene is taken (see column headed “Name of protein identified following a BLASTX analysis of the CuraGen sequence”) as of the filing date of the instant application.

“Polymorphic sequence” provides a 51-base sequence with the polymorphic site at the 26th base in the sequence, as well as 25 bases from the reference sequence on the 5’ side and the 3’ side of the polymorphic site. The designation at the polymorphic site is enclosed in square brackets, and provides first, the reference nucleotide; second, a “slash (/)”; and third, the polymorphic nucleotide. In certain cases the polymorphism is an

insertion or a deletion. In that case, the position which is “unfilled” (i.e., the reference or the polymorphic position) is indicated by the word “gap”.

“Base before” provides the nucleotide present in the reference, or wild-type, gene at the position at which the polymorphism is found.

5 “Base after” provides the altered nucleotide at the position of the polymorphism.

“Amino acid before” provides the amino acid in the reference protein, if the polymorphism occurs in a coding region.

10 “Amino acid after” provides the amino acid in the polymorphic protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses if the polymorphism occurs in a coding region.

“Type of change” provides information on the nature of the polymorphism.

“SILENT-NONCODING” is used if the polymorphism occurs in a noncoding region of a nucleic acid.

15 “SILENT-CODING” is used if the polymorphism occurs in a coding region of a nucleic acid of a nucleic acid and results in no change of amino acid in the translated polymorphic protein.

“CONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in the same class as the reference amino acid. The classes are:

20 Aliphatic: Gly, Ala, Val, Leu, Ile;

Aromatic: Phe, Tyr, Trp;

Sulfur-containing: Cys, Met;

Aliphatic OH: Ser, Thr;

Basic: Lys, Arg, His;

Acidic: Asp, Glu, Asn, Gln;

Pro falls in none of the other classes; and

End defines a termination codon.

5 “NONCONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in a different class than the reference amino acid.

“FRAMESHIFT” relates to an insertion or a deletion. If the frameshift occurs in a coding region, the Table provides the translation of the frameshifted codons 3’ to the polymorphic site.

10 “Protein classification of CuraGen gene” provides a generic class into which the protein is classified. During the course of the work leading to the filing of this application, several classes of proteins were identified. Some are described further below.

15 “Name of protein identified following a BLASTX analysis of the CuraGen sequence” provides the database reference for the protein found to resemble the novel reference-polymorphism cognate pair most closely.

20 “Similarity (pvalue) following a BLASTX analysis” provides the pvalue, a statistical measure from the BLASTX analysis that the polymorphic sequence is similar to, and therefore an allele of, the reference, or wild-type, sequence. In the present application, a cutoff of $pvalue > 1 \times 10^{-50}$ (entered, for example, as 1.0E-50 in the Table) is used to establish that the reference-polymorphic cognate pairs are novel. A $pvalue < 1 \times 10^{-50}$ defines proteins considered to be already known.

“Map location” provides any information available at the time of filing related to localization of a gene on a chromosome.

25 The polymorphisms are arranged in the Table in the following order.

SEQ ID NOs: 1-722 are SNPs that are silent.

SEQ ID NOs: 723-797 are SNPs that lead to conservative amino acid changes.

SEQ ID NOs: 798-989 are SNPs that lead to nonconservative amino acid changes.

5 SEQ ID NOs: 990-1095 are SNPs that involve a gap. With respect to the reference or wild-type sequence at the position of the polymorphism, the allelic cSNP introduces an additional nucleotide (an insertion) or deletes a nucleotide (a deletion). An SNP that involves a gap generates a frame shift.

10 SEQ ID NOs: 1096-1170 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to conservative amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 723-797. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

15 SEQ ID NOs: 1171-1362 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to nonconservative amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 798-989. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the
20 order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

SEQ ID NOs: 1363-1468 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to frameshift-induced amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 990-1095. 7 or 8 amino acids on either
25 side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

Provided herein are compositions which include, or are capable of detecting, nucleic acid sequences having these polymorphisms, as well as methods of using nucleic acids.

IDENTIFICATION OF INDIVIDUALS CARRYING SNPs

5 Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. Strategies for identification and detection are described in *e.g.*, EP 730,663, EP 717,113, and PCT US97/02102. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of
10 polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by *e.g.*, PCR. See generally PCR Technology:
15 Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

20 The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. In particular, as used herein, a recombinantly produced protein relates to the gene product of a polymorphic allele, *i.e.*, a "polymorphic protein" containing an altered amino acid at the site of translation of the nucleotide
25 polymorphism. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The phrase “substantially purified” or “isolated” when referring to a nucleic acid, peptide or protein, means that the chemical composition is in a milieu containing fewer, or preferably, essentially none, of other cellular components with which it is naturally associated. Thus, the phrase “isolated” or “substantially pure” refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as gel electrophoresis or high performance liquid chromatography. Generally, a substantially purified or isolated nucleic acid or protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the nucleic acid or protein is purified to represent greater than 90% of all macromolecular species present. More preferably the nucleic acid or protein is purified to greater than 95%, and most preferably the nucleic acid or protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional analytical procedures.

The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other in vitro amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods P&J 1:25-33 (1992)), prior to mutation analysis.

The method for preparing nucleic acids in a form that is suitable for mutation detection is well known in the art. A “nucleic acid” is a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated. The term “nucleic acids”, as used herein, refers to either DNA or RNA. “Nucleic acid sequence” or “polynucleotide sequence” refers to a single-stranded sequence of deoxyribonucleotide or ribonucleotide

bases read from the 5' end to the 3' end. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 5' end of the RNA transcript in the 5' direction are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 3' end of the RNA transcript in the 3' direction are referred to as "downstream sequences". The term includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence.

10 "Nucleic acid probes" may be DNA or RNA fragments.

The detection of polymorphisms in specific DNA sequences, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl. Acids Res. 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. Sci. USA, 86:6230-6234 (1989)) or oligonucleotide arrays (Maskos and Southern Nucl. Acids Res 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl Acids Res 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox Genome Res 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl Acids Res 23:3944-3948 (1995)), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. Proc. Natl. Acad. Sci. U.S.A. 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. Genomics 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. Science 230:1242 (1985)), chemical (Cotton et al. Proc. Natl. w Sci. U.S.A., 8Z4397-4401 (1988)) or enzymatic (Youil et al. Proc. Natl. Acad. Sci. U.S.A. 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific primer extension (Syvanen et al. Genomics 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. &&I Acids 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. Science 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany Proc. Natl. Acad. Sci. U.S.A. 88:189-193 (1991)), gap-LCR (Abravaya et al. Nucl Acids Res 23:675-682 (1995)), radioactive and/or fluorescent

DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., *Nucl. Acids Res*, 21:5332-5356 (1993); Thiede et al., *Nucl. Acids Res*. 24:983-984 (1996)).

“Specific hybridization” or “selective hybridization” refers to the binding, or duplexing, of a nucleic acid molecule only to a second particular nucleotide sequence to which the nucleic acid is complementary, under suitably stringent conditions when that sequence is present in a complex mixture (e.g., total cellular DNA or RNA). “Stringent conditions” are conditions under which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter ones. Generally, stringent conditions are selected such that the temperature is about 5°C lower than the thermal melting point (T_m) for the specific sequence to which hybridization is intended to occur at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the target sequence hybridizes to the complementary probe at equilibrium. Typically, stringent conditions include a salt concentration of at least about 0.01 to about 1.0 M Na ion concentration (or other salts), at pH 7.0 to 8.3. The temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridization.

“Complementary” or “target” nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe’s length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook et al., or *Current Protocols in Molecular Biology*, F. Ausubel et al., ed., Greene Publishing and Wiley-Interscience, New York (1987).

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion of the target sequence. A "polymorphic" marker or site is the locus at which a sequence difference occurs with respect to a reference sequence. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The reference allelic form may be, for example, the most abundant form in a population, or the first allelic form to be identified, and other allelic forms are designated as alternative, variant or polymorphic alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the "wild type" form, and herein may also be referred to as the "reference" form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two distinguishable forms (i.e., base sequences), and a triallelic polymorphism has three such forms.

As used herein an "oligonucleotide" is a single-stranded nucleic acid ranging in length from 2 to about 60 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides. A probe is an oligonucleotide capable of binding to a target nucleic acid of a complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen bond formation. Oligonucleotides probes are often between 5 and 60 bases, and, in specific embodiments, may be between 10-40, or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in an oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, such as a phosphoramidite linkage or a phosphorothioate linkage, or they may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than by phosphodiester bonds, so long as it does not interfere with hybridization.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a

polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not be perfectly complementary to the exact sequence of the template, but should be sufficiently complementary to hybridize with it. The term "primer site" refers to the sequence of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR. Oligonucleotides for use as primers or probes are chemically synthesized by methods known in the field of the chemical synthesis of polynucleotides, including by way of non-limiting example the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett 22:1859-1 862 (1981) and the triester method provided by Matteucci, et al., J. Am. Chem. Soc., 103:3185 (1981) both incorporated herein by reference. These syntheses may employ an automated synthesizer, as described in Needham-VanDevanter, D.R., et al., Nucleic Acids Res. 12:61596168 (1984). Purification of oligonucleotides may be carried out by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., J. Chrom., 255:137-149 (1983). A double stranded fragment may then be obtained, if desired, by annealing appropriate complementary single strands together under suitable conditions or by synthesizing the complementary strand using a DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The sequence of the synthetic oligonucleotide or of any nucleic acid fragment can be can be obtained using either the dideoxy chain termination method or the Maxam-

Gilbert method (see Sambrook et al. Molecular Cloning - a Laboratory Manual (2nd Ed.), Vols. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al." ; Zyskind et al., (1988)). Recombinant DNA Laboratory Manual, (Acad. Press, New York). Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the SNP-containing nucleotide sequences of the invention, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, about 25, about 50, or about 60 nucleotides or an entire SNP coding strand, or to only a portion thereof.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a polymorphic nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. For example, the antisense nucleic acid molecule can generally be complementary to the entire coding region of an mRNA, but more preferably as

embodied herein, it is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of the mRNA. An antisense oligonucleotide can range in length between about 5 and about 60 nucleotides, preferably between about 10 and about 45 nucleotides, more preferably between about 15 and 40 nucleotides, and still more preferably between about 15 and 30 in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following section).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polymorphic protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementary to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -u nits, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a

complete cDNA or gene sequence. Optimal alignment of sequences for aligning a comparison window may, for example, be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. U.S.A. 852444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

Techniques for nucleic acid manipulation of the nucleic acid sequences harboring the cSNP's of the invention, such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like, are described generally in Sambrook et al., The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein, peptide or amino acid sequence. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein, peptide or amino acid sequence. The nucleic acid sequences include both the full length nucleic acid sequences disclosed herein as well as non-full length sequences derived from the full length protein. It being further understood that the sequence includes the degenerate codons of the native sequence or sequences which may be introduced to provide codon preference in a specific host cell. Consequently, the principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

For assay of genomic DNA, virtually any biological convenient tissue sample can be used. Suitable samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair can be used. Genomic DNA is typically amplified before

analysis. Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. Target is usually labeled in the course of amplification. The amplification product can be RNA or DNA, single stranded or double stranded. If double stranded, the amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with DNase-free RNase.

DETECTION OF POLYMORPHISMS IN A NUCLEIC ACID SAMPLE

The SNPs disclosed herein can be used to determine which forms of a characterized polymorphism are present in individuals under analysis.

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 7, 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in published PCT application WO 95/11995.

WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be
5 complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are
10 expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

An allele-specific primer hybridizes to a site on a target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, Nucleic Acid Res. 17 2427-2448 (1989).
15 This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-
20 base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

Amplification products generated using the polymerase chain reaction can be
25 analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, (W.H. Freeman and Co New York, 1992, Chapter 7).

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989). Amplified PCR products can be generated and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

The genotype of an individual with respect to a pathology suspected of being caused by a genetic polymorphism may be assessed by association analysis. Phenotypic traits suitable for association analysis include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, system, diseases of the nervous and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach, leukemia, liver, lung, and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). Since the polymorphic sites are within a 50,000 bp region in the human genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all 10 polymorphic sites) set forth in this application should be inherited without change for at least several generations. The more sites that are analyzed the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In diallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism are (see WO

95/12607):

$$\text{Homozygote: } p(AA)=x^2$$

$$\text{Homozygote: } p(BB)=y^2=(1-x)^2$$

$$\text{Single Heterozygote: } p(AB)=p(BA)=xy=x(1-x)$$

$$5 \quad \text{Both Heterozygotes: } p(AB+BA)=2xy=2x(1-x)$$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID)=(x^2)^2+(2xy)^2+(y^2)^2.$$

- 10 These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID)=x^4+(2xy)^2+(2yz)^2+(2xz)^2+z^4+y^4$$

- 15 In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($\text{cum } p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus:

$$\text{cum } p(ID)=p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

- 20 The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(nonID)=1-\text{cum } p(ID).$$

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

5 The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in
10 the putative father and the child.

 If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation
15 can be performed to determine the probability of coincidental match.

 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

$$p(exc)=xy(1-xy)$$

20 where x and y are the population frequencies of alleles A and B of a diallelic polymorphic site. (At a triallelic site $p(exc)=xy(1-xy)+yz(1-yz)+xz(1-xz)+3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C). The probability of non-exclusion is:

$$p(non-exc)=1-p(exc)$$

25 The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$cum\ p(non-exc)=p(non-exc1)p(non-exc2)p(non-exc3) \dots p(non-excn)$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded) is:

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic

treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic marker sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of whom exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this

treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., U.S. Pat. No. 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wild type with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered.

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992) (each of which is incorporated by reference in its entirety for all purposes).

Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value

is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction RF , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (RF), ranging from $RF=0.0$ (coincident loci) to $RF=0.50$ (unlinked). Thus, the likelihood at a given value of RF is: probability of data if loci linked at RF to probability of data if loci unlinked. The computed likelihood is usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of RF (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of RF at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of RF) than the possibility that the two loci are unlinked. By convention, a combined lod score of + 3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved

by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. (1989). Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, Science 244, 1288-1292 The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

The invention further provides methods for assessing the pharmacogenomic susceptibility of a subject harboring a single nucleotide polymorphism to a particular pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug-metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug targets have been correlated with individual differences based on distinction in the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmacogenomic characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

In cases in which a cSNP leads to a polymorphic protein that is ascribed to be the cause of a pathological condition, method of treating such a condition includes administering to a subject experiencing the pathology the wild type cognate of the polymorphic protein. Once administered in an effective dosing regimen, the wild type cognate provides complementation or remediation of the defect due to the polymorphic protein. The subject's condition is ameliorated by this protein therapy.

A subject suspected of suffering from a pathology ascribable to a polymorphic protein that arises from a cSNP is to be diagnosed using any of a variety of diagnostic methods capable of identifying the presence of the cSNP in the nucleic acid, or of the cognate polymorphic protein, in a suitable clinical sample taken from the subject. Once the presence of the cSNP has been ascertained, and the pathology is correctable by

administering a normal or wild-type gene, the subject is treated with a pharmaceutical composition that includes a nucleic acid that harbors the correcting wild-type gene, or a fragment containing a correcting sequence of the wild-type gene. Non-limiting examples of ways in which such a nucleic acid may be administered include incorporating the wild-type gene in a viral vector, such as an adenovirus or adeno associated virus, and administration of a naked DNA in a pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. Once the nucleic acid that includes the gene coding for the wild-type allele of the polymorphism is incorporated within a cell of the subject, it will initiate *de novo* biosynthesis of the wild-type gene product. If the nucleic acid is further incorporated into the genome of the subject, the treatment will have long-term effects, providing *de novo* synthesis of the wild-type protein for a prolonged duration. The synthesis of the wild-type protein in the cells of the subject will contribute to a therapeutic enhancement of the clinical condition of the subject.

A subject suffering from a pathology ascribed to a SNP may be treated so as to correct the genetic defect. (See Kren et al., Proc. Natl. Acad. Sci. USA 96:10349-10354 (1999)). Such a subject is identified by any method that can detect the polymorphism in a sample drawn from the subject. Such a genetic defect may be permanently corrected by administering to such a subject a nucleic acid fragment incorporating a repair sequence that supplies the wild-type nucleotide at the position of the SNP. This site-specific repair sequence encompasses an RNA/DNA oligonucleotide which operates to promote endogenous repair of a subject's genomic DNA. Upon administration in an appropriate vehicle, such as a complex with polyethylenimine or encapsulated in anionic liposomes, a genetic defect leading to an inborn pathology may be overcome, as the chimeric oligonucleotides induces incorporation of the wild-type sequence into the subject's genome. Upon incorporation, the wild-type gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair.

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For

example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100, 1000 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the hybridizing methods.

Several aspects of the present invention rely on having available the polymorphic proteins encoded by the nucleic acids comprising a SNP of the inventions. There are various methods of isolating these nucleic acid sequences. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences complementary to the sequences disclosed herein.

Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known, See Gubler, U. and Hoffman, B.J. *Gene* 25:263-269 (1983) and Sambrook et al.

For a genomic library, for example, the DNA is extracted from tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, et al. Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, *Science* 196:180-182 (1977). Colony hybridization is carried out as generally described in M. Grunstein et al. *Proc. Natl. Acad. Sci. USA.* 72:3961-3965 (1975). DNA of interest is identified in either cDNA or

genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, et al.

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired. PCR can be used in a variety of protocols to isolate cDNAs encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from the sequence.

Once DNA encoding a sequence comprising a cSNP is isolated and cloned, one can express the encoded polymorphic proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain initiation sequences, transcription and translation terminators, and promoters useful for regulation of the expression of a polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for

translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook et al.

A variety of prokaryotic expression systems may be used to express the polymorphic proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacterial. 158:1018-1024 (1984) and the leftward promoter of phage lambda as described by A, I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol. See Sambrook et al. for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503. Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

Any of a variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, may also be used to express a polymorphic protein of the

invention. As explained briefly below, a nucleotide sequence harboring a cSNP may be expressed in these eukaryotic systems. Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., et al., Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, et al., Gene 8:17-24 (1979); Broach, et al., Gene 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glucanase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, Nature (London) 275:104-109 (1978); and Hinnen, A., et al., Proc. Natl. Acad. Sci. USA, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., et al., J. Bact, 153:163-168 (1983)) cells and applying standard protein isolation techniques to the lysates.

The purification process can be monitored by using Western blot techniques or radioimmunoassay or other standard techniques. The sequences encoding the proteins of the invention can also be ligated to various immunoassay expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g.,

the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen et al. Immunol. Rev. 89:49 (1986)) and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences.

5 Other animal cells are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)). Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from baculovirus. Insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider J. Embryol. Exp. Morphol., 27:353-365 (1987). As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences. As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known

10 mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, J. et al., J. Virol. 45: 773-781 (1983)). Additionally, gene sequences to control replication in the host cell may be

15 Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238. The host cells are competent or rendered competent for transformation by various means. There are several well-known methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the

20 recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or

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as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein “operably linked” refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. Specifically, “operably linked” means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the gene encoding the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression sequence. The term “vector”, refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids.

The term “gene” as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term “gene” is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, termination regions and similar untranslated nucleotide sequences. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A43 1 cells, human Co10205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL- 60, U937, HaK or Jurkat cells. Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains,

Candida or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac© kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed." The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein.

The polymorphic protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein. The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art.

The polymorphic proteins produced by recombinant DNA technology may be purified by techniques commonly employed to isolate or purify recombinant proteins. Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide. The polypeptides of this invention may be purified to substantial purity by standard

techniques well known in the art, including selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, Protein Purification: Principles and Practice, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an
5 embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

The resulting expressed protein may then be purified from such culture (i.e.,
10 from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-Toyopearl@ or Cibacrom blue 3GA Sepharose B; one or more steps involving hydrophobic interaction
15 chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography. Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such
20 fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT). Finally, one or more reverse-phase high performance liquid chromatography (RP-
25 HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance
30 with the present invention as an "isolated protein."

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as polymorphic. Such antibodies include, but are not limited to, polyclonal,
5 monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human polymorphic proteins are disclosed.

The phrase "specifically binds to", "immunospecifically binds to" or is "specifically immunoreactive with", an antibody when referring to a protein or peptide,
10 refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biological materials. Thus, for example, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody
15 that is selected for its specificity for a particular protein. Of particular interest in the present invention is an antibody that binds immunospecifically to a polymorphic protein but not to its cognate wild type allelic protein, or vice versa. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select
20 monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) Antibodies, a Laboratory Manual, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

Polyclonal and/or monoclonal antibodies that immunospecifically bind to
25 polymorphic gene products but not to the corresponding prototypical or "wild-type" gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, Antibodies, A Laboratory Manual, Cold Spring Harbor Press, New York (1988); Goding, Monoclonal antibodies, Principles
30 and Practice (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are

tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product.

An isolated polymorphic protein, or a portion or fragment thereof, can be used as an immunogen to generate the antibody that binds the polymorphic protein using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polymorphic protein can be used or, alternatively, the invention provides antigenic peptide fragments of polymorphic for use as immunogens. The antigenic peptide of a polymorphic protein of the invention comprises at least 8 amino acid residues of the amino acid sequence encompassing the polymorphic amino acid and encompasses an epitope of the polymorphic protein such that an antibody raised against the peptide forms a specific immune complex with the polymorphic protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of polymorphic that are located on the surface of the protein, *e.g.*, hydrophilic regions.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the polymorphic protein. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polymorphic protein or a chemically synthesized polymorphic polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against polymorphic proteins can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography, to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that originates from the clone of a singly hybridoma cell, and that contains only one type of antigen binding site capable of immunoreacting with a particular epitope of a polymorphic protein. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polymorphic protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular polymorphic protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a polymorphic protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methodologies can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a polymorphic protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polymorphic protein may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-polymorphic protein antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988) *J Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060.

In one embodiment, methodologies for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art.

Anti-polymorphic protein antibodies may be used in methods known within the art relating to the detection, quantitation and/or cellular or tissue localization of a polymorphic protein (*e.g.*, for use in measuring levels of the polymorphic protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for polymorphic proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody-derived CDR, are utilized as pharmacologically-active compounds in therapeutic applications intended to treat a pathology in a subject that arises from the presence of the cSNP allele in the subject.

An anti-polymorphic protein antibody (*e.g.*, monoclonal antibody) can be used to isolate polymorphic proteins by a variety of immunochemical techniques, such as

immunoaffinity chromatography or immunoprecipitation. An anti-polymorphic protein antibody can facilitate the purification of natural polymorphic protein from cells and of recombinantly produced polymorphic proteins expressed in host cells. Moreover, an anti-polymorphic protein antibody can be used to detect polymorphic protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polymorphic protein. Anti-polymorphic antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance.

Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that unique compositions and methods of use thereof in SNPs in known genes have been described. Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims which follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims.

WHAT IS CLAIMED IS:

1. An isolated polynucleotide selected from the group consisting of:
 - a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468;
 - 5 b) a fragment of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
 - c) a complementary nucleotide sequence comprising a sequence complementary to one or more of said polymorphic sequences selected from the group consisting of SEQ ID NOS:1-1468; and
 - 10 d) a fragment of said complementary nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.
2. The polynucleotide of claim 1, wherein said polynucleotide sequence is DNA.
- 15 3. The polynucleotide of claim 1, wherein said polynucleotide sequence is RNA.
4. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 100 nucleotides in length.
- 20 5. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 90 nucleotides in length.
6. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 75 nucleotides in length.
- 25 7. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and about 50 bases in length.
8. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and about 40 bases in length.
- 30

9. The polynucleotide of claim 1, wherein said polynucleotide is between about 15 and about 30 bases in length.
10. The polynucleotide of claim 1, wherein said polymorphic site includes a nucleotide other than the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
11. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of said polymorphic sequence.
12. The polynucleotide of claim 1, wherein said polymorphic site includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
13. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes the complement of the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
14. An isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is selected from the group consisting of:
- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468 provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence;
 - b) a nucleotide sequence that is a fragment of said polymorphic sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
 - c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468, provided that the

complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

15. The oligonucleotide of claim 14, wherein the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide selected from the group consisting of:

- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468, wherein said polymorphic sequence includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence;
- b) a nucleotide sequence that is a fragment of any of said nucleotide sequences;
- c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468, wherein said polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and
- d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

16. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 51 bases in length.

17. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 40 bases in length.

18. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 15 and about 30 bases in length.

19. A method of detecting a polymorphic site in a nucleic acid, the method comprising:

- a) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
- b) determining whether said nucleic acid and said oligonucleotide hybridize;

whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphic site in said nucleic acid.

20. The method of claim 19, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

21. The method of claim 19, wherein said oligonucleotide is between about 10 and about 51 bases in length.

22. The method of claim 19, wherein said oligonucleotide is between about 10 and about 40 bases in length.

23. A method of detecting the presence of a sequence polymorphism in a subject, the method comprising:

- a) providing a nucleic acid from said subject;
- b) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
- c) determining whether said nucleic acid and said oligonucleotide hybridize;

whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphism in said subject.

24. A method of determining the relatedness of a first and second nucleic acid, the method comprising:

- a) providing a first nucleic acid and a second nucleic acid;
- b) contacting said first nucleic acid and said second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;
- c) determining whether said first nucleic acid and said second nucleic acid hybridize to said oligonucleotide; and
- d) comparing hybridization of said first and second nucleic acids to said oligonucleotide, wherein hybridization of first and second nucleic acids to said nucleic acid indicates the first and second subjects are related.

25. The method of claim 24, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide

recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

- 5 26. The method of claim 24, wherein the oligonucleotide is between about 10 and about 51 bases in length.
27. The method of claim 24, wherein the oligonucleotide is between about 10 and about 40 bases in length.
- 10 28. The method of claim 24, wherein the oligonucleotide is between about 15 and about 30 bases in length.
- 15 29. An isolated polypeptide comprising a polymorphic site at one or more amino acid residues, wherein the protein is encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-1468, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the
- 20 nucleotide recited in Table 1, column 5.
- 25 30. The polypeptide of claim 29, wherein said polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.
- 30 31. The polypeptide of claim 29, wherein the polypeptide encoded by said polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

32. An antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

33. The antibody of claim 32, wherein said antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

34. The antibody of claim 32, wherein said antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

35. A method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject, the method comprising

- a) providing a protein sample from said subject;
- b) contacting said sample with the antibody of claim 34 under conditions that allow for the formation of antibody-antigen complexes; and
- c) detecting said antibody-antigen complexes,

whereby the presence of said complexes indicates the presence of said polypeptide.

36. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

- a) providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence

selected from the group consisting of SEQ ID NOS:1 - 1468, or its complement; and

- b) administering to the subject an effective therapeutic dose of a second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele,

thereby treating said subject.

37. The method of claim 36, wherein the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

38. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

- a) providing a subject suffering from a pathology associated with aberrant expression of a polymorphic sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1 - 1468, or its complement; and

- b) administering to the subject an effective therapeutic dose of a polypeptide,

wherein said polypeptide is encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

39. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or its complement; and

b) administering to the subject an effective dose of the antibody of claim 34,

thereby treating said subject.

40. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or its complement; and

b) administering to the subject an effective dose of an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for said polymorphic sequence,

thereby treating said subject.

41. An oligonucleotide array, comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is chosen from the group consisting of:

a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468;

b) a nucleotide sequence that is a fragment of any of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;

c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468; and

d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

42. The array of claim 41, wherein said array comprises about 10 oligonucleotides.

43. The array of claim 41, wherein said array comprises about 100 oligonucleotides.

44. The array of claim 41, wherein said array comprises about 1000 oligonucleotides.

ABSTRACT

The invention provides nucleic acids containing single-nucleotide polymorphisms
5 identified for transcribed human sequences, as well as methods of using the nucleic acids.

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| | | | | | | | | | | | | |
|----|------------|------|---|---|-----|--|--|----------------------|------------------|---|----------|-----------------|
| 7 | cg43988460 | 4708 | TACCAAAAAAAAA AAAGGAAAGGA AA[G/A]AAAGG GTGGCCTGACA CTGGTGCC | G | A | | | SILENT- NONCODING | cadherin | Human Gene SWISSPROT- ID:P19022 NEURAL-CADHERIN PRECURSOR (N-CADHERIN) - HOMO SAPIENS (HUMAN), 906 aa. | 0.00E+00 | 18 (18q11.2) |
| 8 | cg43982945 | 460 | GACACATGTCA GGCTGGGCGAG CAG[C/gap]CACT CTGATCAGCAC CAGGTCCCGA | C | gap | | | SILENT- NONCODING | cathepsin | Human Gene Similar to SWISSPROT- ID:Q26534 CATHEPSIN L PRECURSOR (EC 3.4.22.15) (SMCL1) - SCHISTOSOMA MANSONI (BLOOD FLUKE), 319 aa. | 2.00E-80 | 11 |
| 9 | cg43266931 | 96 | GGGCGCTAGCG GGGGTGACCGG CGG[G/gap]CCG GTAGGCCGCCA GGATCTCGGCG | G | gap | | | SILENT- NONCODING | chloride channel | Human Gene Similar to SWISSNEW- ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa. pds:SWISSPROT-ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa. | 3.10E-59 | 9 |
| 10 | cg43321451 | 1126 | GAAGGCACACA CACACACACAC ACA[C/gap]AGCA AAAGCTAAATCA TCACCCGCG | C | gap | | | SILENT- NONCODING | collagen | Human Gene SWISSPROT- ID:Q99715 COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa. pds:SPTREMBL-ID:Q99715 COLLAGEN TYPE XII ALPHA-1 PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa. | 0.00E+00 | 6 |
| 11 | cg43933757 | 3195 | TCATCTCCCTGC AACCTCCGCCT CC[T/C]GGGTTT AAGCGATTCTTG TGCCTCA | T | C | | | SILENT- NONCODING | complement | Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa. | 0.00E+00 | 5 (5p13) |
| 12 | cg43933757 | 3212 | CCGCCTCCTGG GTTCAAGCGATT CTT[C/GTGCCT CAGCCTCCCAA GCAGCTGG | T | C | | | SILENT- NONCODING | complement | Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa. | 0.00E+00 | 5 (5p13) |

| | | | | | | | | | | | | | |
|----|------------|------|---|---|-----|--|--|--|----------------------|----------------|---|-----------|----------|
| 13 | cg43933757 | 3346 | TCCAACCTCCTGA CCTCAGGTAATC C[G/A]CCTGCCT TGGCCTCCCAA AGTGCTG | G | A | | | | SILENT- NONCODING | complem ent | Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa. | 0.00E+00 | 5 (5p13) |
| 14 | cg42185571 | 2224 | CTTAGCTCTACG ATTAAATCCAT G[T/gap]GTCCAA GGGGGAAACA TATTATAT | T | gap | | | | SILENT- NONCODING | complem ent | Human Gene SWISSPROT- ID:P02748 COMPLEMENT COMPONENT C9 PRECURSOR - HOMO SAPIENS (HUMAN), 559 aa. | 7.70E-308 | 5 (5p13) |
| 15 | cg42185571 | 2367 | TAATATAGATAG TGTTCACTAGCA G[A/gap]ATAGAA TGAACATAAACT ATTAGTT | A | gap | | | | SILENT- NONCODING | complem ent | Human Gene SWISSPROT- ID:P02748 COMPLEMENT COMPONENT C9 PRECURSOR - HOMO SAPIENS (HUMAN), 559 aa. | 7.70E-308 | 5 (5p13) |
| 16 | cg43947909 | 265 | GAATTGTCCAGA AGACTTGGCTC AGC/TJTGAGG AGCTGATAGAC ATGGCTGT | C | T | | | | SILENT- NONCODING | complem ent | Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q- R PROTEIN) (HYALURONAN- BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa. | 6.9E-129 | 17 |

| | | | | | | | | | | | | |
|----|------------|------|---|---|-----|--|--|----------------------|----------------|---|----------|---------------|
| 17 | cg43143315 | 2860 | GTGTGTGTGTCT GTGTGTGTGTG TC[C/G]GTGTAT GTGTGTGTGGG TTCTAATG | C | G | | | SILENT- NONCODING | cyto450 | Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lpcis:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa. | 1.9E-279 | 20 |
| 18 | cg43327428 | 1746 | AGCAGGCTGGC CTATGTGGTCTA AG[A/G]TTCAGC CTGAAACTCATA GACACTG | A | G | | | SILENT- NONCODING | cyto450 | Human Gene SWISSNEW-ID:P04798 CYTOCHROME P450 1A1 (EC 1.14.14.1) (CYP1A1) (P450-P1) (P450 FORM 6) (P450-C) - HOMO SAPIENS (HUMAN), 512 aa.lpcis:SWISSPROT-ID:P04798 CYTOCHROME P450 1A1 (EC 1.14.14.1) (P450-P1) (P450 FORM 6) (P450-C) (TCDD-INDUCIBLE) - HOMO SAPIENS (HUMAN).512 aa. | 2.5E-279 | 15 (15q22) |
| 19 | cg32296860 | 376 | CAGCACTTTGG GAGGCCGAGGC GGG[T/C]GGATC ACCCGAGGTCA GGAGTTCCA | T | C | | | SILENT- NONCODING | cytochro me | Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment). | 6.6E-124 | |
| 20 | cg32296860 | 383 | TTGGGAGGCCG AGCGGGGTGGA TCA[C/gap]CCGA GGTCAGGAGTT CGAGACCAGC | C | gap | | | SILENT- NONCODING | cytochro me | Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment). | 6.6E-124 | |

| | | | | | | | | | | | | | |
|----|------------|-----|--|---|-----|-----|--|--|----------------------|---------------|---|-----------|----|
| 21 | cg32296860 | 385 | GGGAGGCCGAG GCGGGTGGATC ACC[C/gap]GAG GTCAGGAGTTC GAGACCGCCT | C | | gap | | | SILENT- NONCODING | cytochrome | Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment). | 6.6E-124 | |
| 22 | cg32296860 | 397 | CGGGTGGATCA CCCGAGGTCAG GAGT[A]TCGAG ACGAGCCTGGC CAACATGGT | T | A | | | | SILENT- NONCODING | cytochrome | Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment). | 6.60E-124 | |
| 23 | cg32296860 | 439 | CAACATGGTGA AACCCTGTCTCT AC[T/C]AAAAATA CAAAAATTAGCT GGGTGC | T | C | | | | SILENT- NONCODING | cytochrome | Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment). | 6.60E-124 | |
| 24 | cg43264442 | 199 | GGGGCGCGGGT GGAGAACTGC GGC[A/G]GCGCG GCCCCGTAGGAA GGTGCTGTC | A | G | | | | SILENT- NONCODING | dehydrogenase | Human Gene TREMBLNEW- ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT {EC 1.1.1.22} - BOS TAURUS, 468 aa. | 8.60E-240 | 4 |
| 25 | cg43264442 | 236 | AGGAAGGTGCT GTCCGAACGAT CGG[G/A]ATAGG AGCGGTCCCTG CGCTTGCTG | G | A | | | | SILENT- NONCODING | dehydrogenase | Human Gene TREMBLNEW- ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT {EC 1.1.1.22} - BOS TAURUS, 468 aa. | 8.60E-240 | 4 |
| 26 | cg43998926 | 130 | GAACCCAAAGAG CCACTGATAACT GG[C/gap]ACAAT CCAATGAAACA GAGGAAGCA | C | gap | | | | SILENT- NONCODING | dehydrogenase | Human Gene SWISSPROT- ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa. | 1.30E-190 | 15 |

| | | | | | | | | | | | | | |
|----|------------|-----|--|---|---|--|--|--|----------------------|-------------------|---|------------------------|----|
| 27 | cg43998926 | 560 | CTCAGGCTGAG TTGCCTCCAAGTC TTT/GJGGAATG TCATCTTATACT GGTACTG | T | G | | | | SILENT- NONCODING | dehydrog enase | Human Gene SWISSPROT- ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa. | 1.30E-190 | 15 |
| 28 | cg43941594 | 499 | GGTTATAAAAT AGATAACTCGCA G/A/GJGTCATAA ATATCTACAGTT AGTAGA | A | G | | | | SILENT- NONCODING | dehydrog enase | Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL- 3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa. | 1.90E-137 | 3 |
| 29 | cg43962927 | 462 | GCCACTCCCTG CTCCCTGCCTG AGC/G/AJCCATT CGCAGTCTTGTT TCCTGTTT | G | A | | | | SILENT- NONCODING | dna_rna _bind | Human Gene SWISSPROT- ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) HOMO SAPIENS (HUMAN), 993 aa. | 0.00E+00 (11q13.2) | 11 |
| 30 | cg43991661 | 671 | CTTGTTTATTAT CTATCATAGACA T/C/GJAAGATGA TCATAGTTAATA CCAATT | C | G | | | | SILENT- NONCODING | dna_rna _bind | Human Gene TREMBLNEW- ID:G2058493 TELOMERIC REPEAT DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 419 aa. | 5.10E-224 | 8 |
| 31 | cg43991661 | 737 | ACTGTTTATAGGC CCAATATTGATA T/A/GJTAAATGA AGGTATCAGAG AATCTT | A | G | | | | SILENT- NONCODING | dna_rna _bind | Human Gene TREMBLNEW- ID:G2058493 TELOMERIC REPEAT DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 419 aa. | 5.10E-224 | 8 |
| 32 | cg43310449 | 206 | CTAAAGATTTC TGTCCTCAGTGG A/A/GJCTGGCAT ACTGTAATTGCT ATGTGG | A | G | | | | SILENT- NONCODING | dynein | Human Gene SWISSPROT- ID:Q63100 DYNEIN INTERMEDIATE CHAIN 1, CYTOSOLIC (DH IC-1) - RATTUS NORVEGICUS (RAT), 643 aa. | 1.0e-312 | |
| 33 | cg43310449 | 231 | ACTGGCATACT GTAATTGCTATG TG[G/A]AAGCTTAA TATAACCTCAAC AGCAGC | G | A | | | | SILENT- NONCODING | dynein | Human Gene SWISSPROT- ID:Q63100 DYNEIN INTERMEDIATE CHAIN 1, CYTOSOLIC (DH IC-1) - RATTUS NORVEGICUS (RAT), 643 aa. | 1.0e-312 | |

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|----|------------|------|--|---|---|--|--|--|----------------------|------------------|--|--------------------|---------------|
| 34 | cg43984524 | 1227 | TCAATGAGGCTT TCTATTAATTC CTT/CJTAAAAGC AATGGTTATTAT TGAAA | T | C | | | | SILENT- NONCODING | esterase | Human Gene Similar to SPTREMBL- ID:P70665 SIALIC ACID-SPECIFIC 9- O-ACETYLESTERASE - MUS MUSCULUS (MOUSE), 541 aa. | 3.2E-99 | |
| 35 | cg43248101 | 2516 | GGCCCTGAATG TTATGAAGGTTT GA/GA/GTCAGC CTACAGATAACA GGATTAT | G | A | | | | SILENT- NONCODING | fgf | Human Gene Homologous to SWISSPROT-ID:P21781 KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST GROWTH FACTOR- 7) (FGF-7) (HBGF-7) - HOMO SAPIENS (HUMAN), 194 aa. | 9.30E-106 | 15 (15q15) |
| 36 | cg43974968 | 2973 | CAGTGGCTCAC GCCTATAATCCC AG/C/AJACTTTG GGAGGCCAAGG CAGGAGGA | C | A | | | | SILENT- NONCODING | fgf | Human Gene Homologous to SPTREMBL-ID:P78443 21 KD BASIC FIBROBLAST GROWTH FACTOR (BFGF) - HOMO SAPIENS (HUMAN), 196 aa. | 1.70E-103 4 (Xq26) | |
| 37 | cg43074195 | 222 | CAGCTGAAGGA GATAATTGGTGT GA/A/G/CAGAAG CTGAAAGCTTCT AATGGAG | A | G | | | | SILENT- NONCODING | glycoprot ein | Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.40E-197 | 1 |
| 38 | cg43074195 | 237 | ATTGGTGTGAAC AGAAAGCTGAAA GCT/AJTCTAATG GAGACACTCCT ACACATG | T | A | | | | SILENT- NONCODING | glycoprot ein | Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.40E-197 | 1 |
| 39 | cg43074195 | 246 | AACAGAAAGCTG AAAGCTTCTAAT GG/A/GIGACACT CCTACACATGAA GACTTGA | A | G | | | | SILENT- NONCODING | glycoprot ein | Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.40E-197 | 1 |
| 40 | cg43074195 | 255 | TGAAAGCTTCTA ATGGAGACACT CC/T/AJACACAT GAAGACTTGAC CAAGAACA | T | A | | | | SILENT- NONCODING | glycoprot ein | Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.40E-197 | 1 |

| | | | | | | | | | | | | | |
|----|------------|------|--|---|-----|--|--|--|----------------------|--------------|---|----------|---|
| 41 | cg43988092 | 658 | TAGCGATACAAA TATATATATATAT [A/gap]TTTATCC AAAAATATGTTT TATACA | A | gap | | | | SILENT- NONCODING | glycoprotein | Human Gene SWISSPROT- ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa. | 4E-192 | 8 |
| 42 | cg43953517 | 2457 | AAGTTCTTGTAG TAGGTAGGGG TA[C/T]TACTAGG GATATCTGTGG CATGATT | C | T | | | | SILENT- NONCODING | glycoprotein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |
| 43 | cg43953517 | 2464 | TGTAGTAGGTA GGGGGTACTAC TAG[G/C]GATAT CTGTGGCATGA TTATGCAIT | G | C | | | | SILENT- NONCODING | glycoprotein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |
| 44 | cg43953517 | 2491 | ATATCTGTGGCA TGATTATGCATT C[C/gap]GTAGTA TTATTTAAATTAAT TTGGGG | C | gap | | | | SILENT- NONCODING | glycoprotein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |
| 45 | cg43953517 | 2517 | GTAGTATTATT AATTAATTTGGG G[T/G]TCATTTTG CTTCCTTTTCTT TATGC | T | G | | | | SILENT- NONCODING | glycoprotein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |
| 46 | cg43953517 | 2529 | AATTAATTTGGG GTTCAATTTTGCT T[C/gap]CTTTTC TTTATGCTTAGA TTATCTT | C | gap | | | | SILENT- NONCODING | glycoprotein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |
| 47 | cg43953517 | 2530 | ATTAATTTGGGG TTCATTTTGCTT C[C/gap]TTTTCT TTATGCTTAGAT TATCTTA | C | gap | | | | SILENT- NONCODING | glycoprotein | Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa. | 2.9E-150 | 4 |

| | | | | | | | | | | | | |
|----|------------|------|--|---|-----|--|--|----------------------|--------------|---|---------|-----------------|
| 48 | cg43290087 | 1150 | CCTAACCTCTTG GTAACGGTAGT CC[T/C]GAGAGT TCGCAGTGTC A GTGAAATC | T | C | | | SILENT- NONCODING | glycoprotein | Human Gene Similar to SWISSPROT- ID:P52166 MEMBRANE PROTEIN SEL-12 - CAENORHABDITIS ELEGANS, 461 aa. | 1.7E-97 | 14 (14q24.3) |
| 49 | cg43294632 | 913 | AGTAGAGAGTA GGGGTAAAGC TGG[A/G]CATTG CAAAAGGATTG GTTTAAGAA | A | G | | | SILENT- NONCODING | glycoprotein | Human Gene Similar to SWISSNEW- ID:Q13361 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN 2 PRECURSOR (MAGP-2) (MP25) - HOMO SAPIENS (HUMAN), 173 aa. pcis:SWISSPROT-ID:Q13361 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 2 PRECURSOR (MAGP-2) - HOMO SAPIENS (HUMAN), 173 aa. | 4.3E-92 | 12 |
| 50 | cg43056971 | 884 | GTTATTTGAAAA ATACCTATTTTT T[T/gap]CCAAAG TGTGTAAAGAT TGTTTTG | T | gap | | | SILENT- NONCODING | glycoprotein | Human Gene Similar to SPTREMBL- ID:O04711 P-GLYCOPROTEIN-2 - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 1233 aa. | 2.2E-72 | 1 |
| 51 | cg43976227 | 212 | TTCATGTGCAAG CTAAGTTATTCC T[C/A]TGGTCAAT CCTCTCCATCTT CTGGT | C | A | | | SILENT- NONCODING | glycoprotein | Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 2.6E-60 | 18 |
| 52 | cg43994600 | 1782 | CCTTGTTCCAC TCTCCTTCATAT C[C/T]AAGTCAT CAACATCTGAA TGAGAG | C | T | | | SILENT- NONCODING | helicase | Human Gene Similar to SWISSNEW- ID:O70133 ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) (MHEL-5) - MUS MUSCULUS (MOUSE), 1380 aa. pcis:TREMBLNEW-ID:G2961456 RNA HELICASE A - MUS MUSCULUS (MOUSE), 1380 aa. | 8.7E-67 | 14 |

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|----|------------|------|---|---|---|--|--|----------------------|------------|---|---|---|
| 53 | cg43925670 | 2481 | ATGTTCTTGTAT TTTTTCCCATC TTTCTACAGACA TAAGTGAGCCT CACTGG | T | C | | | SILENT- NONCODING | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0 | 1 |
| 54 | cg43925670 | 2488 | TGTATTTTTC CCATCTTTACAG A/C/TJATAAGTGA GCCTCACTGGA AATTTT | C | T | | | SILENT- NONCODING | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0 | 1 |
| 55 | cg43925670 | 2501 | CATCTTTACAGA CATAAGTGAGC CTCTJACTGGA AATTTTTCAC AGTAGTC | C | T | | | SILENT- NONCODING | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0 | 1 |

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|----|------------|------|---|---|--|--|--|----------------------|----------------|---|---|---|
| 56 | cg43925670 | 2507 | TACAGACATAAG A TGAGCCTCACT GG[A/G]AATTTT TCAACAGTAGTC CAGATC | G | | | | SILENT- NONCODING | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.jpcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0 | 1 |
| 57 | cg43925670 | 2513 | CATAAGTGAGC T CTCACTGGAAT TTT[C/T]TCAACA GTAGTCCAGAT CTTGAGA | C | | | | SILENT- NONCODING | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.jpcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0 | 1 |
| 58 | cg43925670 | 2551 | CCAGATCTTGA C GATCTTCAGAAA TG[C/T]AGGAAT CAATGCTTATTT GTGTGAG | T | | | | SILENT- NONCODING | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.jpcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0 | 1 |

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|----|------------|------|--|---|-----|--|--|----------------------|----------------------|---|----------|-----------------|
| 59 | cg42489232 | 2434 | ATTTTGTAGTAGA GACAAAGTTTGTG CCTTATGTTGG CCAGGCTGGTC TCGAACT | C | T | | | SILENT- NONCODING | interferon | Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2) - HOMO SAPIENS (HUMAN), 515 aa. | 3.9E-281 | 21 (21q22.1) |
| 60 | cg42489232 | 2441 | GTAGAGACAAG GTTTGGCCATGT TG[G/C]CCAGGC TGGTCTCGAACT CCTGACC | G | C | | | SILENT- NONCODING | interferon | Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2) - HOMO SAPIENS (HUMAN), 515 aa. | 3.9E-281 | 21 (21q22.1) |
| 61 | cg42489232 | 2454 | TTTGCCATGTTG GCCAGGCTGGT CTC[T/G]AACTC CTGACCTCAAG CGATCOGC | C | T | | | SILENT- NONCODING | interferon | Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2) - HOMO SAPIENS (HUMAN), 515 aa. | 3.9E-281 | 21 (21q22.1) |
| 62 | cg43926168 | 694 | GAAGGGCTCTC CTTCACGGGA CTG[A/gap]AAAA AAAAAATCATGA AATCCTAAT | A | gap | | | SILENT- NONCODING | interleukin receptor | Human Gene Similar to SWISSPROT- ID:P18510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL- 1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa. | 8.8E-94 | 2 (2q14.2) |
| 63 | cg43926168 | 704 | CCTTCACGGGG ACTGAAAAAAA AA[A/gap]TCATG AAATCCTAATTT TCATTTTC | A | gap | | | SILENT- NONCODING | interleukin receptor | Human Gene Similar to SWISSPROT- ID:P18510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL- 1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa. | 8.8E-94 | 2 (2q14.2) |

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|----|------------|------|--|---|---|--|--|----------------------|--------|--|-----------|----|
| 64 | cg43336163 | 2889 | AGCCGGGAATG CTGCTGCTGCT GCT[G]A]CTGCT GCTGCTGCTGC TGGGGGGAT | G | A | | | SILENT- NONCODING | kinase | Human Gene TREMBLNEW- ID:G300258 MYOTONIC DYSTROPHY KINASE, DM-KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa. | 0 | 19 |
| 65 | cg43987164 | 1043 | AGGCGAGCCCC TCAGAAGCCTTC CC[G]A]GCAGAT CCGGGGACCCCC GTTCTGGT | G | A | | | SILENT- NONCODING | kinase | Human Gene TREMBLNEW- ID:D1023392 INOSITOL 1,4,5- TRISPHOSPHATE 3-KINASE ISOENZYME (EC 2.7.1.127) - HOMO SAPIENS (HUMAN), 604 aa (fragment). | 1.3E-307 | |
| 66 | cg43119489 | 2227 | TTTTTCATCCTA TCAATTGAATGT G[G]C]CTTGAAA AATCCAGCAAG AGCGGGG | G | C | | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00537 SERINE/THREONINE- PROTEIN KINASE PCTAIRE-2 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 523 aa. | 2.7E-282 | |
| 67 | cg43957170 | 2164 | CTACTAAAATA CAAAAAATTAGC C[G]A]GGCGTGG TGGCGCATGCC TGTAATC | G | A | | | SILENT- NONCODING | kinase | Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa. | 1.7E-234 | |
| 68 | cg43957170 | 2175 | ACAAAAAATTAG CCGGGCGTGGT GG[C]T]GCATGC CTGTAGTCCCA GCTACTCG | C | T | | | SILENT- NONCODING | kinase | Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa. | 1.70E-234 | |
| 69 | cg43957170 | 2179 | AAAATTAGCCG GGCGTGGTGGC GCA[T]C]GCCTG TAGTCCCAGCTA CTCGGGAG | T | C | | | SILENT- NONCODING | kinase | Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa. | 1.70E-234 | |

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|----|------------|------|---|---|-----|--|--|--|----------------------|--------|---|-----------|----|
| 70 | cg38438124 | 1767 | ACTTTGTGTATA TGTGTGTGTGT GT[G/gap]TGTGT GGGGGGGGTGA GTGTGTGCG | G | gap | | | | SILENT- NONCODING | kinase | Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa. | 2.80E-216 | 10 |
| 71 | cg38438124 | 1769 | TTTGTGTATATG TGTGTGTGTGT GT[G/gap]TTGGG GGGGGTGAGT GTGTGCGCG | G | gap | | | | SILENT- NONCODING | kinase | Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa. | 2.80E-216 | 10 |
| 72 | cg42923882 | 123 | AGTGGGCAGGG ACCCTGGGAGC CTC[C/A]ATTCTC AATGCCCCACC CTTTACCT | C | A | | | | SILENT- NONCODING | kinase | Human Gene SPTREMBL-ID:Q92961 MAP KINASE KINASE MEK5B - HOMO SAPIENS (HUMAN), 448 aa. | 1.80E-196 | |
| 73 | cg43948037 | 1031 | AAAGTTCTCGAA ATGCTTCATCCC C[G/A]ACAAAGC AAATTTCATGTC CGTCAG | G | A | | | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa. | 6.10E-189 | |
| 74 | cg43948037 | 1106 | CTGTTGCTTTCC CTGGGGGTGTCC AG[G/A]CTCACC AGGGGAGTCAG AATCTTCT | G | A | | | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa. | 6.10E-189 | |

| | | | | | | | | | | | | | |
|----|------------|------|---|---|-----|--|--|--|----------------------|--------|--|-----------|----|
| 75 | cg43948037 | 1115 | TCCCTGGGGTG TCCAGGCTCAC CAG[G]GGAGT CAGAATCTTCTG GTTCTCCC | G | C | | | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa. | 6.10E-189 | |
| 76 | cg43948037 | 1124 | TGTCCAGGCTC ACCAGGGGAGT CAG[A]GATCTT CTGGTTCTCCCT TTTCATCA | A | G | | | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa. | 6.10E-189 | |
| 77 | cg43948037 | 1134 | CACCAGGGGAG TCAGAAATCTTCT GG[T]CTCTCCC TTTTCATCAAGT CTTCTAA | T | C | | | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa. | 6.10E-189 | |
| 78 | cg42703622 | 2409 | TGTGGGTTGAC AGATTTTAAAA TA[G/C]AATTTAG AGTATTGGGGT TTTGT | G | C | | | | SILENT- NONCODING | kinase | Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa. | 3.00E-187 | 12 |
| 79 | cg43336176 | 5568 | TGCTGCTGCTG CTGCTGCTGGG GGG[G/gap]ATCA CAGACCATTCT TTCTTCGG | G | gap | | | | SILENT- NONCODING | kinase | Human Gene SPTREMBL-ID:Q16205 MYOTONIN PROTEIN KINASE - HOMO SAPIENS (HUMAN), 625 aa. | 1.10E-164 | 19 |
| 80 | cg43982923 | 610 | ACGCAGGGGTC CCCGCGGCCGC CGC[G/A]ATGCA GAAATACGAGA AACTGGA | G | A | | | | SILENT- NONCODING | kinase | Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa. | 3.60E-159 | 19 |

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|----|------------|------|--|---|---|--|--|--|----------------------|--------------------|---|-----------|----|
| 81 | cg43265203 | 688 | ACATTCAAGCTC GGTGTGTTTCA C[A/C]CGCGTGC GCCCGGCTGC GGCGGTG | A | C | | | | SILENT- NONCODING | kinase | Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA- 1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.pcls:SWISSPROT- ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa. | 5.50E-124 | |
| 82 | cg43966625 | 77 | CGCTGCCCGCG CGGGGACACACA ACC[A/C]AAGTC GCGCGCGCCGC AGCCATGCG | A | C | | | | SILENT- NONCODING | kinase | Human Gene Similar to SWISSPROT- ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa.pcls:SPTREMBL- ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa. | 3.20E-89 | 17 |
| 83 | cg44004317 | 4772 | CACCACGATGC GGACCCCACTG CCC[G/A]GCTCG ACCTCCTCGGG AGGGGGGCG | G | A | | | | SILENT- NONCODING | kinasere ceptor | Human Gene SWISSNEW-ID:P04626 ERBB-2 RECEPTOR PROTEIN- TYROSINE KINASE PRECURSOR (EC 2.7.1.112) (P185ERBB2) (NEU PROTO-ONCOGENE) (C-ERBB-2) - HOMO SAPIENS (HUMAN), 1255 aa.pcls:SWISSPROT-ID:P04626 ERBB-2 RECEPTOR PROTEIN- TYROSINE KINASE PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1255 aa. | 0.00E+00 | |
| 84 | cg43925424 | 300 | TCGGGCGACAG TCGCTGCTCCG CGC[G/T]CGCGC CCGGCGGCGCT CCAGGTGCT | G | T | | | | SILENT- NONCODING | kinesin | Human Gene SWISSPROT- ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa. | 1.90E-304 | 14 |

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|----|------------|------|--|---|-----|--|--|----------------------|-------------|--|-----------|----------|
| 94 | cg43967268 | 598 | ACGAGAAAGG AGCAGCTGAA GTG[G]CCTGG ACTCCAGCCCT GGCTGTTGT | G | A | | | SILENT- NONCODING | oncogene | Human Gene Similar to SWISSPROT- ID:P24407 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 207 aa. | 1.90E-52 | |
| 95 | cg43920534 | 1076 | CGTCACTATGTA CTTGGTTTTGCG CT[<i>gap</i>]TTTTTTT CCTTAAAAAAA AAGGCC | T | gap | | | SILENT- NONCODING | phosphatase | Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa. | 0.00E+00 | 12 |
| 96 | cg43920534 | 763 | CTTCATAAAACC AATCGAGAGAG AG[A] <i>gap</i> GGACT TAAATCCTGCT TACCAAAA | A | gap | | | SILENT- NONCODING | phosphatase | Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa. | 0.00E+00 | 12 |
| 97 | cg43926887 | 1786 | ATTGTTTTCAAC ATGAAGTAAAGA A[T]A[A]ACGTTGA GGCCTTTACTAT TAGCT | T | A | | | SILENT- NONCODING | phosphatase | Human Gene SWISSPROT- ID:Q06190 PROTEIN PHOSPHATASE PP2A, 130 KD REGULATORY SUBUNIT (PR130) - HOMO SAPIENS (HUMAN), 1150 aa. | 0.00E+00 | 3 |
| 98 | cg43926887 | 1838 | GTCTAATACTCC TGGGAGGAAGG AA[T]A]ATATCTA TCTAGTAAGAAT TTTAAT | T | A | | | SILENT- NONCODING | phosphatase | Human Gene SWISSPROT- ID:Q06190 PROTEIN PHOSPHATASE PP2A, 130 KD REGULATORY SUBUNIT (PR130) - HOMO SAPIENS (HUMAN), 1150 aa. | 0.00E+00 | 3 |
| 99 | cg43088901 | 2303 | GAGCACCGTGT CAAGCTGCTCT GAG[C/T]CACAG TGGGATGAACC AGCCGGGGC | C | T | | | SILENT- NONCODING | phosphatase | Human Gene SWISSNEW-ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa. ipdls:SWISSPROT-ID:P30304 M- PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa. | 4.00E-288 | 3 (3p21) |

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|-----|------------|------|--|---|-----|--|--|----------------------|-------------------|---|-----------|----|
| 100 | cg43920213 | 3664 | GTGAGCCATAAT ATGATGGCCAG CA[G/gap]GTGG CGCTGCCCTTCC ACCCATGGTG | G | gap | | | SILENT- NONCODING | phosphatase | Human Gene Similar to SWISSPROT- ID:P51452 DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR) - HOMO SAPIENS (HUMAN), 185 aa. | 6.00E-81 | 17 |
| 101 | cg43969348 | 648 | TGGGGGAAATG GGCCTCTTGGG GGT[C/gap]TCAC TGCACGGCTTG TTCATTGGCA | C | gap | | | SILENT- NONCODING | polymrase | Human Gene Similar to SPTREMBL- ID:Q15370 RNA POLYMERASE II TRANSCRIPTION FACTOR SIII P18 SUBUNIT - HOMO SAPIENS (HUMAN), 118 aa. | 3.90E-59 | 16 |
| 102 | cg43966692 | 331 | TACGAATTGGCA TATTTGTTTATTT [C/gap]TCAGTTT GTGAAAATGTCC TTAATT | C | gap | | | SILENT- NONCODING | polymrase | Human Gene Similar to SPTREMBL- ID:Q15369 RNA POLYMERASE II ELONGATION FACTOR SIII, P15 SUBUNIT - HOMO SAPIENS (HUMAN), 112 aa. | 4.00E-57 | 8 |
| 103 | cg43265754 | 4375 | CGAGACCAGCC TGGCCAACATG GTG[A/C]AACC CATCTCTACTAA AAATACAA | A | C | | | SILENT- NONCODING | potassium_channel | Human Gene SWISSPROT- ID:P48544 G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL 4 (GIRK4) (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 5) (HEART KATP CHANNEL) (KATP-1) (CARDIAC INWARD RECTIFIER) (CIR) (KIR3.4) - HOMO SAPIENS (HUMAN), 419 aa. | 6.70E-185 | |
| 104 | cg43265754 | 4389 | CCAACATGGTG AAACCCCATCTC TA[C/T]TAAAAAT ACAAAAATTAGC CGGGCG | C | T | | | SILENT- NONCODING | potassium_channel | Human Gene SWISSPROT- ID:P48544 G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL 4 (GIRK4) (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 5) (HEART KATP CHANNEL) (KATP-1) (CARDIAC INWARD RECTIFIER) (CIR) (KIR3.4) - HOMO SAPIENS (HUMAN), 419 aa. | 6.70E-185 | |

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|-----|------------|------|---|---|-----|--|--|----------------------|---------------|---|-----------|-----------------|
| 105 | cg43922227 | 538 | ATGTTGTGTTGG GTCCCCAGATT CC[C/T]ATTGAT TTTCTTGCATCA TTTTCT | C | | | | SILENT- NONCODING | reductas e | Human Gene Homologous to SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa. | 7.70E-150 | 14 |
| 106 | cg43927549 | 1020 | GTAAGCAGCAC ACTAGGAGGCC CAG[G/gap]CGC AGGCAAAGAGA AGATGGTGCTG | G | gap | | | SILENT- NONCODING | reductas e | Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa. | 1.60E-124 | 6 (6pter) |
| 107 | cg43957486 | 4041 | TGTATCATAGAA ATGTAACITTTTG T[A/G]AGACAAA GGTTTTCCTCTT CTATTT | A | G | | | SILENT- NONCODING | struct | Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa. | 0.00E+00 | 20 (20p11.2) |
| 108 | cg43973080 | 779 | GACACTAGGAA TTTCTTAAAAAG AA[A/gap]GATGT TGGAAGCAGAA CACTTACTA | A | gap | | | SILENT- NONCODING | struct | Human Gene TREMBLNEW- ID:G2304981 MYOSIN VI - HOMO SAPIENS (HUMAN), 1262 aa. | 0.00E+00 | 6 |
| 109 | cg42914441 | 2306 | CTCTGACCTGA GTCITTTGTTTA AG[A/G]AGTATTT GTCITCCTTTGT CTAATG | A | G | | | SILENT- NONCODING | struct | Human Gene Homologous to SWISSPROT-ID:P26044 RADIXIN (MOESIN B) - SUS SCROFA (PIG), 583 aa. | 5.40E-133 | 22 (22q12.2) |
| 110 | cg43942318 | 1006 | GGACACCCCTCG GACCCTCGAAA ACG[C/T]CTCAG GAGCTATGAAG ACATGATTG | C | T | | | SILENT- NONCODING | struct | Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa. | 4.80E-123 | 11 |

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|-----|------------|------|---|---|-----|--|--|----------------------|----------|---|-----------|----|
| 111 | cg43929933 | 431 | CAGGCCAGGCC TGTTGTCTCCAC CTG[C/G]ACAGG CATTCTCCTTGT TCCAGAAA | C | G | | | SILENT- NONCODING | struct | Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa. | 1.80E-117 | 12 |
| 112 | cg43929933 | 541 | CGCAGCCCCAA GTGTCAACAAG GGG[C/T]TCAAT AAGGCTTTCTG GGAGCCACT | C | T | | | SILENT- NONCODING | struct | Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa. | 1.80E-117 | 12 |
| 113 | cg43929933 | 590 | CTGGCAGCTGG TGGGATGGAAG GGG[G/gap]AGG TGGAAAAGGGC AGAGGAAATGG | G | gap | | | SILENT- NONCODING | struct | Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa. | 1.80E-117 | 12 |
| 114 | cg43070037 | 7268 | AGGTCAGGAGT TTGAGACCAGC CTA[G/A]CCAAC ATGGTGAAACC CCATCTCTA | G | A | | | SILENT- NONCODING | synthase | Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYC NAMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa. | 0.00E+00 | |

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| 115 | cg43070037 | 7269 | GGTCAGGAGTT TGAGACCAGCC TAGC/GJCAACA TGGTGAACCC CATCTCTAC | C | G | | | | SILENT- NONCODING | synthase | Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa. | 0.00E+00 | |
| 116 | cg43070037 | 7352 | GIGGGTGCCTG TAATCCCAGCTA CTC/TJGGGAGG CTGAGGCAGGA GAATCACC | C | T | | | | SILENT- NONCODING | synthase | Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa. | 0.00E+00 | |
| 117 | cg43070037 | 7365 | ATCCCAGCTACT CGGGAGGCTGA GGC/TJAGGAGA ATCACCTGAACC TAGGAGG | C | T | | | | SILENT- NONCODING | synthase | Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa. | 0.00E+00 | |

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|-----|------------|------|--|---|-----|--|--|--|----------------------|------------------|--|-----------|----|
| 118 | cg43070037 | 7366 | TCCAGCTACTCA | A | G | | | | SILENT- NONCODING | synthase | Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa. | 0.00E+00 | |
| 119 | cg43123664 | 240 | AGTACGCCAGC CCGGGGCGGCC CCG A/C ATGTA CATGTTCCACG CGGGATTCC | A | C | | | | SILENT- NONCODING | synthase | Human Gene Similar to SWISSPROT- ID:O35696 ALPHA-2,8- SIALYLTRANSFERASE (EC 2.4.99.-) (ST8SIAI) (SIALYLTRANSFERASE X) (STX) (POLYSIALIC ACID SYNTHASE) - MUS MUSCULUS (MOUSE), 375 aa. | 3.10E-59 | 18 |
| 120 | cg21428405 | 17 | NACGCGTTGGC GTCGTT/C CTC GTTGAGCTCATC AATCCACCAC | T | C | | | | SILENT- NONCODING | synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.20E-56 | |
| 121 | cg43982633 | 811 | ACACAGCCCCA GTTTGCTTTACA GC[C/G]CAAGTT ACAAACTGTCCC TTTTAAA | C | G | | | | SILENT- NONCODING | tgfrecept or | Human Gene SWISSPROT- ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR- ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa. | 1.50E-254 | |
| 122 | cg43054268 | 312 | TCTAGATATTTA ACTGACCCACTA T[A/gap]TTCCTC AAGGATACTGC ATTGGAC | A | gap | | | | SILENT- NONCODING | thioester ase | Human Gene Similar to TREMBLNEW-ID:E307161 MITOCHONDRIAL VERY-LONG- CHAIN ACYL-COA THIOESTERASE - RATTUS NORVEGICUS (RAT), 453 aa. | 3.50E-83 | 9 |

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|-----|------------|------|---|---|-----|--|--|----------------------|------------------|---|-----------|----------|
| 123 | cg43054268 | 448 | GACTATATGATC AAAGCCCTTAG C[A]gap]AAAAAA ATTTTAAATATT TGCAAA | A | gap | | | SILENT- NONCODING | thioester ase | Human Gene Similar to TREMBLNEW-ID:E307161 MITOCHONDRIAL VERY-LONG- CHAIN ACYL-COA THIOESTERASE - RATTUS NORVEGICUS (RAT), 453 aa. | 3.50E-83 | 9 |
| 124 | cg43943775 | 259 | TGAAGATTACCC CCACACCTGTG TG[A]G]CAAGTG ATCAAAAAAGGAA CAGGACC | A | G | | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P21554 CANNABINOID RECEPTOR 1 (CB1) (CB-R) (CANN6) - HOMO SAPIENS (HUMAN), 472 aa. | 5.40E-252 | 6 (6q14) |
| 125 | cg42886565 | 3473 | GGCAACAAAAAG CGAAACTCCATC TC[A]gap]AAAA AAAGAGCTATAG GATCTTTA | A | gap | | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa. | 4.40E-225 | 5 (5q13) |
| 126 | cg42886565 | 3481 | AAGCGAAACTC CATCTCAAAAA AA[A]gap]GAGCT ATAGGATCTTTA CAATATAI | A | gap | | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa. | 4.40E-225 | 5 (5q13) |
| 127 | cg42886565 | 4462 | TCCTCTGTCTGC TGGCTGGCCGC GT[G]A]TATGAA GAAGACTAATTG GACACAG | G | A | | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa. | 4.40E-225 | 5 (5q13) |
| 128 | cg42886565 | 4483 | GCGTGTATGAA GAAGACTAATTG GA[C]T]ACAGAG CCGTGATGAATT AAAGTCT | C | T | | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa. | 4.40E-225 | 5 (5q13) |
| 129 | cg43307001 | 1796 | GCCTCCCGGGT TCAAGTGATTCT CC[T]C]GCCTCA GCCTCCCAGTA GCTGGGAT | T | C | | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa. | 2.50E-199 | |

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|-----|------------|------|--|---|-----|--|--|----------------------|-----|---|-----------|----|
| 130 | cg43307001 | 1898 | GGGGTTTCACC ATGTTGGCCAG GCT[G/A]GTCTC GAACTCCTGAC CTCAAGTGA | G | A | | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa. | 2.50E-199 | |
| 131 | cg43307001 | 1909 | ATGTTGGCCAG GCTGGTCTCGA ACT[C/T]CTGAC CTCAAGTGATCC GCCACCT | C | T | | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa. | 2.50E-199 | |
| 132 | cg43047341 | 2113 | GGTGGATCACC TGAGGTCACGA GTT[C/T]GAGAC CAGCCTGACCA ACATGGAGA | C | T | | | SILENT- NONCODING | tm7 | Human Gene SWISSPROT- ID:P21731 THROMBOXANE A2 RECEPTOR (TXA2-R) (PROSTANOID TP RECEPTOR) - HOMO SAPIENS (HUMAN), 369 aa. | 2.80E-190 | |
| 133 | cg43965652 | 891 | TCCATTCTTTT TCTTTTTTTTTT [T/gap]TAAGTGA GACTACATTGG CAAATGG | T | gap | | | SILENT- NONCODING | tnf | Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa. | 4.50E-121 | 16 |
| 134 | cg43965652 | 892 | CCATTCTTTT CTTTTTTTTTTT [T/gap]AAGTGAG ACTACATTGGCA AATGGG | T | gap | | | SILENT- NONCODING | tnf | Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa. | 4.50E-121 | 16 |
| 135 | cg43965652 | 412 | TTCCAAACATCA AATGAAGGGG AT[C/gap]AATGG TTACCACTATCG TTTTCAAC | C | gap | | | SILENT- NONCODING | tnf | Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa. | 4.50E-121 | 16 |
| 136 | cg43985709 | 933 | AGCTCACTTTGG CCCTTCTCCACC C[A/G]TCCCAAC CCCAATTGCTAAC AACATG | A | G | | | SILENT- NONCODING | tnf | Human Gene Similar to SWISSPROT- ID:Q13829 TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) - HOMO SAPIENS (HUMAN), 316 aa. | 1.70E-51 | 16 |

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|-----|------------|------|---|---|-----|--|--|--|----------------------|----------------------|---|-----------|---------------|
| 144 | cg43917396 | 915 | TAGGGGCTGAA ACGCAGTCGGG GCC[G/gap]GGC ACTGCCCAGGA AGGGACTCCGG | G | gap | | | | SILENT- NONCODING | transcript factor | Human Gene Similar to TREMBLNEW-ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 HOMO SAPIENS (HUMAN), 518 aa. | 6.90E-68 | |
| 145 | cg43949162 | 510 | TAGACAATACCA TCTCTAGGAACA C[A/G]CTGTCAC TCACACATGGAT GTGTG | A | G | | | | SILENT- NONCODING | transferase | Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa. | 1.30E-115 | 6 |
| 146 | cg41653463 | 2407 | TGTGCGTGCGT GTGTGTGTGTG TGT[G/gap]TGTA TCGTGTGTGTGT GTTTTGTTT | G | gap | | | | SILENT- NONCODING | transport | Human Gene SWISSPROT- ID:P31641 SODIUM- AND CHLORIDE-DEPENDENT TAURINE TRANSPORTER - HOMO SAPIENS (HUMAN), 620 aa. | 0.00E+00 | 3 (3p25) |
| 147 | cg41653463 | 2408 | TGTGCGTGCGTG TGTTGTGTGTGT GTGT[G/gap]GTAT CGTGTGTGTGT GTTTTGTTT | T | gap | | | | SILENT- NONCODING | transport | Human Gene SWISSPROT- ID:P31641 SODIUM- AND CHLORIDE-DEPENDENT TAURINE TRANSPORTER - HOMO SAPIENS (HUMAN), 620 aa. | 0.00E+00 | 3 (3p25) |
| 148 | cg43285429 | 388 | CCCAGTCAAGA TAAGGAGGATC CCA[G/A]CAGCT CCCCTCCGAGG TTGGGCTCT | G | A | | | | SILENT- NONCODING | transport | Human Gene SWISSNEW-ID:P02730 BAND 3 ANION TRANSPORT PROTEIN (ANION EXCHANGE PROTEIN 1) (AE 1) - HOMO SAPIENS (HUMAN), 911 aa.lpcis:SWISSPROT-ID:P02730 BAND 3 ANION TRANSPORT PROTEIN (ANION EXCHANGE PROTEIN 1) (AE 1) - HOMO SAPIENS (HUMAN), 911 aa. | 0.00E+00 | 17 (17q21) |
| 149 | cg43918636 | 3322 | AGCAGCAGCTG TTGGAGTAGAA CCG[C/A]GTCCA GGGCGCGACCA TC TTCATCG | C | A | | | | SILENT- NONCODING | transport | Human Gene Similar to SWISSPROT- ID:Q15012 GOLGI 4- TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108) - HOMO SAPIENS (HUMAN), 233 aa. | 5.40E-52 | |

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|-----|------------|------|--|-----|-----|--|--|--|----------------------|------------------|---|-----------|----|
| 150 | cg44005525 | 721 | TAAGCAGCTCTC TTCTGTGACAGA C[A]gapJAATCAT GTAAGAACTGT GAAACCCC | A | gap | | | | SILENT- NONCODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 | |
| 151 | cg44005525 | 743 | GACAAATCATGT AAGAACTGTGAA A[C]A]CCAGTT TATGTAGCGTAT CTCTTG | C | A | | | | SILENT- NONCODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 | |
| 152 | cg40986905 | 3075 | ATTTTATAGTAG GACGGGGTTTC AC[C]T]GTGTTA GCCAGGATGGT CTCGATCT | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14162 KIAA0149 PROTEIN - HOMO SAPIENS (HUMAN), 830 aa. | 0.00E+00 | |
| 153 | cg43303871 | 1999 | AATAAGGGGAGA ACTACTATTTTT TT[gap/]JAAGAT CTCAAAATAATT AATAATAA | gap | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA25444 KIAA0518 PROTEIN - HOMO SAPIENS (HUMAN), 650 aa (fragment). | 0.00E+00 | |
| 154 | cg43303871 | 1999 | AATAAGGGGAGA ACTACTATTTTT TT[gap/]JAAGAT CTCAAAATAATT AATAATAA | gap | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA25444 KIAA0518 PROTEIN - HOMO SAPIENS (HUMAN), 650 aa (fragment). | 0.00E+00 | |
| 155 | cg43918386 | 3972 | CTTCTACCCCAT GGGTAAATGTAT TT[C]ACATATTA CCAAGAGAAGA AGCACA | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14511 ENHANCER OF FILAMENTATION 1 - HOMO SAPIENS (HUMAN), 834 aa. | 0.00E+00 | 6 |
| 156 | cg43923712 | 501 | AGGAATCCTGG ACAGGAGTTTTTC TG[C/]JAGAGGC GTTTAAACCCCT ACCGAAT | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q12996 CLEAVAGE STIMULATION FACTOR 77KDA SUBUNIT - HOMO SAPIENS (HUMAN), 717 aa. | 0.00E+00 | 11 |

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|-----|------------|-------|---|---|-----|--|--|--|----------------------|------------------|---|----------|---------------------|
| 157 | cg43936083 | 189 | GCTAACTGGTG ACAGTTATAAAA AC[A/G]CAAAAA GGAGCCTGGGA AACAGCAA | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa. | 0.00E+00 | |
| 158 | cg43936393 | 382 | AAAAACAAGTTT CAGTAAAAA A[A/gap]ACTAAA ACAAACACTGAA GTAGAGT | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR- ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa. | 0.00E+00 | 17 |
| 159 | cg43936393 | 383 | AAAAACAAGTTTC AGTAAAAA A[A/gap]CTAAAA CAAACACTGAA GTAGAGTT | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR- ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa. | 0.00E+00 | 17 |
| 160 | cg43940465 | 304 | ACTGTATTATTT ATTACATGGGC T[G/A]AAAGCAA AGAAAAATGAGT CCCTTC | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60300 KIAA0553 PROTEIN - HOMO SAPIENS (HUMAN), 1095 aa (fragment). | 0.00E+00 | |
| 161 | cg43940880 | 10186 | TAGTTTGTAAAG ACTGTACAAAA A[A/gap]TGCTTC TGGAGATTTCCTT TGGCAGA | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P53794 SODIUM/MYO- INOSITOL COTRANSPORTER (NA(+)/MYO-INOSITOL COTRANSPORTER) - Homo sapiens (Human), 718 aa. | 0.00E+00 | 21 |
| 162 | cg43950657 | 1956 | TTTGGGATCCTG ATCAATTCTTTC T[G/A]ATGTTGTT GAAAATGACAAA GTTGG | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa. | 0.00E+00 | 21 (21q22.1) |

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|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|--|----------|---------------------|
| 163 | cg43950657 | 2033 | CAGCTGCCAAA ACCGTGTGTGC AAG[A/G]GCGCG ACCTAAGGGGA CATTCTTGT | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa. | 0.00E+00 | 21 (21q22.1) |
| 164 | cg43973740 | 485 | TGAAGCAAAACAA ACAAACAAAAA A[A/gap]GGAGAG CTTCATTAGTAG CCAAGAT | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q61123 MATERNAL EMBRYONIC MESSAGE 3 (MEM3) - MUS MUSCULUS (MOUSE), 754 aa. | 0.00E+00 | 16 (12q12) |
| 165 | cg43980521 | 1011 | GCGCATGGGTC CCTCCAGGAAG GCT[T/G]GGTTA GAGTCCCAGGG TGGTCCCCA | T | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA20795 KIAA0337 PROTEIN - HOMO SAPIENS (HUMAN), 1510 aa. | 0.00E+00 | 11 |
| 166 | cg43980521 | 551 | CCCTCAGCTTTG GGGGTCCTTC CT[G/A]AAGGGG CTTCCCTTGCA GAAGGGG | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA20795 KIAA0337 PROTEIN - HOMO SAPIENS (HUMAN), 1510 aa. | 0.00E+00 | 11 |
| 167 | cg43980521 | 873 | AGCATCTTGATC TAGAGGACTGA GG[G/A]CAGCCC CATCAGGCTGG GGCCCTGG | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA20795 KIAA0337 PROTEIN - HOMO SAPIENS (HUMAN), 1510 aa. | 0 | 11 |
| 168 | cg44019839 | 3287 | AGCTACACAGA GGAATAACTTA GGT[C/J]ACTTTCT GTTTTTTAAAA AAAATA | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q99743 NEURONAL PAS DOMAIN PROTEIN 2 (NEURONAL PAS2) (MEMBER OF PAS PROTEIN 4) (MOP4) - Homo sapiens (Human), 824 aa. | 0 | |

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|-----|------------|------|--|---|---|--|--|--|----------------------|------------------|--|----------|---|
| 169 | cg44021891 | 787 | AGAAGACCTGG CTTCTTACAAC AG[G/A]GACAGG CTGGTGGCTGG GGCTAGAG | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa. | 0 | 3 |
| 170 | cg44021891 | 869 | GCCCCCAGCTA GGACCCTGTAG TTG[G/A]GACCG TGGCATGATACA AGGACCTG | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa. | 0 | 3 |
| 171 | cg44921773 | 2876 | TTCTGAGACAG GGTCTTGCTCT GTC[G/A]CCCCAG GCTGGAGTGCA ATGGCACGA | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13471 REPLICATION CONTROL PROTEIN 1 - HOMO SAPIENS (HUMAN), 861 aa. | 0 | 1 |
| 172 | cg44921773 | 2955 | GGGCTCAAGTG ATCCTCCACCT CA[A/G]CCTCCC GAGTAGCTGAG ACTACAGG | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13471 REPLICATION CONTROL PROTEIN 1 - HOMO SAPIENS (HUMAN), 861 aa. | 0 | 1 |
| 173 | cg43961485 | 650 | GGTCTCCTCAG TGGTCTATTTTA GG[T/G]GTGGTT TTTTTTTTTTTT TTACTG | T | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60398 TXBP151 - HOMO SAPIENS (HUMAN), 563 aa. | 1.5E-303 | 7 |
| 174 | cg43985955 | 2111 | GAGCACAGATA CAGTTTATGTAA CTT[A/G]ATGGA AGAAAATGGAAT TACTCCA | T | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.7E-299 | |
| 175 | cg44916647 | 1142 | GCTCAGCAGCC CCTAGGAAGTTA AG[C/T]GAGAGC TACAGGGCAGG GGGGCTCC | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa. | 4.3E-299 | 1 |

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|-----|------------|------|--|---|-----|--|--|--|----------------------|------------------|---|----------|----|
| 176 | cg44916647 | 494 | TCTGTACATGTA ACATGTGGCCA TG[C/gap]CCAGG CATCCAGCAT CTATCCTGA | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa. | 4.3E-299 | 1 |
| 177 | cg44021459 | 2082 | GGTCACTGTTTC CTCGGCATCGT GC[T/C]GCCCTGG AGAGAACTCCC GACCGGGA | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAC16046 FIP2 - HOMO SAPIENS (HUMAN), 577 aa. | 1E-297 | |
| 178 | cg43926814 | 372 | TAGAATTTTCTA TCCCCCCCCATT T[C/T]TCCAGTAA TAAAAAGTAGTG CTGGG | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA- 62) - Homo sapiens (Human), 536 aa. | 5E-289 | 14 |
| 179 | cg43926814 | 412 | GTAGTGCTGGG ATCTGGCACCC AGA[T/C]TTGGTT TTTATCCTGACC ATTACA | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA- 62) - Homo sapiens (Human), 536 aa. | 5E-289 | 14 |
| 180 | cg43931431 | 1415 | AGCCATGTACG TGAAATTGCTTG GG[A/T]ACCTGA ACTCCCGCTGG AATTCTA | A | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q14154 HYPOTHETICAL PROTEIN KIAA0141 - Homo sapiens (Human), 515 aa. | 7.2E-281 | 5 |
| 181 | cg44031765 | 277 | ATGCACCTGGC CCACATGGCTG GGC[G/A]CTGCA GCCTGCACCTCC ACTTCCAGG | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa. | 4.6E-279 | 22 |
| 182 | cg44031765 | 4030 | CATCTTTATAGG CCACCACTGTG TG[C/T]TTGCTG CGCCGGGCACC CACGAACT | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa. | 4.6E-279 | 22 |

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|-----|------------|------|--|---|-----|--|--|----------------------|------------------|--|-----------|----|
| 183 | cg43970492 | 331 | TGCTTTGTTGCT TCAAGATGCATG C[A/C]ATCCTG GCTTAGTGTC AAGTAT | A | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa. | 3.60E-270 | 22 |
| 184 | cg42847874 | 1118 | ACAAAATTAGC CGGGCATGGT GC[G/A]CAGCC TGAGTCCCAG CTACTTAG | G | A | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA34492 KIAA0772 PROTEIN HOMO SAPIENS (HUMAN), 468 aa. | 6.30E-258 | 20 |
| 185 | cg43951020 | 534 | GAGTGCAGTG CTCACTGCAAC CTC[C/T]GCCCTC CCAGGTTCAAG CAATTCCTCC | C | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O76021 PBK1 PROTEIN - HOMO SAPIENS (HUMAN), 516 aa. | 6.60E-255 | |
| 186 | cg43951020 | 552 | CAACCTCCGCC TCCCAGGTTCAA GC[A/G]ATTCTC CTGCCTCAGCC TCCCTAGT | A | G | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O76021 PBK1 PROTEIN - HOMO SAPIENS (HUMAN), 516 aa. | 6.60E-255 | |
| 187 | cg43971614 | 2720 | ACCAATTGCTTG GTCAATTCAACC TG[A/J]GGGGAA AAGAGTCAAATA TGTCCTA | G | A | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 5.30E-253 | 5 |
| 188 | cg43971614 | 2802 | CTCTGCACCCAC AGCACCGAGGA TAG[T/C]ACAAA CCCCTCACGCG TCTGCGTCC | T | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 5.30E-253 | 5 |
| 189 | cg43962954 | 192 | CGGGCTCCCCA TGCAGCCCTAG AGA[C/gap]GGG AGAAAGTCCAGT GTGCTGTTCCA | C | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa. | 4.80E-252 | 19 |

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|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|---|-----------|----|
| 190 | cg43917689 | 1684 | AGGCAACACCT GTGAGGAAGG GCACTTGGGGC AAAAGCTCACCT CAGAAAGTG | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa. | 3.50E-240 | 3 |
| 191 | cg43917685 | 2176 | TCAGATGACTTT ACAACCAAGG AGT/CIACACAG GGCAACAACAA ATTAGAGG | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment). | 2.50E-230 | 14 |
| 192 | cg43287642 | 307 | GCAACTTATTT AAAACCCAAAG GA[G/A]AAAGGA TGGTACTACCAT AAATCAC | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD20347 NEBULIN - HOMO SAPIENS (HUMAN), 977 aa (fragment). | 3.50E-224 | |
| 193 | cg43986954 | 1072 | AGTGGAAACATT TTTGTTCATTT CT/CJAGGAATTT TCTCTTGGGA AAGTCG | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAC68871 METHYL-CPG BINDING PROTEIN MBD2 - HOMO SAPIENS (HUMAN), 411 aa. | 9.40E-224 | 18 |
| 194 | cg42882543 | 3078 | TCCCGAGTAGC TGGGATTACAG GCA[T/C]GCGCC ACCACGCCCCAG CTAATTTTT | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75177 KIAA0693 PROTEIN - HOMO SAPIENS (HUMAN), 404 aa (fragment). | 2.30E-220 | |
| 195 | cg43062833 | 1567 | TGAAAAGTATTA TGGAAATCACTG C[A/T]GCACAGG AAAAGTAATTCA GATGTT | A | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q93088 BETAINE-- HOMOCYSTEINE S- METHYLTRANSFERASE (EC 2.1.1.5) - Homo sapiens (Human), 406 aa. | 2.10E-219 | 5 |
| 196 | cg43959148 | 342 | AGACTAGTGTG GGCCTTGGGCC CCC[C/gap]TCAT TTTGACATCCTT CCAGATGGT | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75955 FLOTILLIN-1 - HOMO SAPIENS (HUMAN), 427 aa. | 1.40E-215 | 6 |

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|-----|------------|------|--|---|-----|--|--|--|----------------------|------------------|---|-----------|---------------|
| 197 | cg43950766 | 385 | GTTCACATTTAG TGAACCTGCATT TTC/gap/JATGGGG GGGGGGGGGG TACACAGTA | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD44491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa. | 5.30E-214 | 22 |
| 198 | cg43958860 | 1340 | TCTGTCTTTTAT TTAACAAAAAT GTC/JAATTAAT GTAAACTTGGAA TCAAG | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P48745 NOV PROTEIN HOMOLOG PRECURSOR (NOVH) - Homo sapiens (Human), 357 aa. | 6.00E-206 | 8 (8q24.1) |
| 199 | cg43968205 | 1516 | CTATAGCAGAG GGGGTTATGGG GGC[G/A]GGAGG GTAGACTGACAT ACAGAAAGT | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB46373 HYPOTHETICAL 71.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 653 aa (fragment). | 6.90E-206 | |
| 200 | cg43950996 | 825 | ACGCCAGTCCA GAAAGAAGGTG CTG[G/A]AGCCC CTGCTCTGTCCT CTCCATCA | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa. | 6.20E-204 | 1 |
| 201 | cg44924222 | 1787 | TAAGGGTGAGC AGCAGCAGGAG CGC[A/T]TTGAA GAAGAAAGTAGA AGGGGATGT | A | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1) - Homo sapiens (Human), 372 aa. | 2.7E-203 | |
| 202 | cg44924222 | 1834 | ATGTCAGGCAC CGTGCGCAGAC TGC[A/G]GTGAC TGGTGGCATAAC AGGACCTTG | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1) - Homo sapiens (Human), 372 aa. | 2.7E-203 | |
| 203 | cg44924222 | 2073 | GTACCGGAAGG CGTAGGAGGAG ACG[A/G]TTGAGG ATGAGAGTGAC CACGTGGTG | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1) - Homo sapiens (Human), 372 aa. | 2.7E-203 | |

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|-----|------------|------|--|-----|---|--|--|----------------------|------------------|---|----------|---|
| 204 | cg44916575 | 1943 | GAGGACAAAA CAGAAAGCCCT GTG[AT]GTGTG GGAAAACTCCG CTGCAGAGA | A | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q16842 BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.4) (CMP-N- ACETYLNEURAMINATE-BETA- GALACTOSAMIDE-ALPHA-2,3- SIALYL-TRANSFERASE) - HOMO SAPIENS (HUMAN), 350 aa. | 3.7E-197 | |
| 205 | cg42650960 | 2321 | GGCTGGAGTGC AGTGGCACGAT CTC[G/A]GCTCA CTGCAAGCCTC CGCCTCCCG | G | A | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q10981 GALACTOSIDE 2-L- FUCOSYLTRANSFERASE 2 (EC 2.4.1.69) (GDP-L-FUCOSE:BETA-D- GALACTOSIDE 2-ALPHA-L- FUCOSYLTRANSFERASE 2) (ALPHA(1,2)FT 2) (FUCOSYLTRANSFERASE 2) (SECRETOR BLOOD GROUP ALPHA-2- FUCOSYLTRANSFERASE) (SECRETOR FACTOR) (SE) (SE2) - Homo sapiens (Human), 343 aa. | 2E-189 | |
| 206 | cg43947129 | 2163 | CTGGGGGCGTC CATGGTGC GGC GGC[G/C]JAGGGC GGTGAGTCAGC CAAGGAGGA | G | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EP1P) - Oryctolagus cuniculus (Rabbit), 370 aa. | 3E-188 | |
| 207 | cg43922383 | 199 | ATCTGAAAAATGG TGTTGTGGCGTC GC[G/A]JCGGCC AGCTATCGTCA GTGCCCTTT | G | A | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |
| 208 | cg43922383 | 222 | CGCGGCCAGC TATCGTCAGTGC CT[gap/G]TTATT GCCATTGGGTTT GTGACTGT | gap | G | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |

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|-----|------------|------|--|---|-----|--|--|--|----------------------|------------------|--|-----------|----|
| 209 | cg43922383 | 239 | TCAGTGCCTTTA TTGCCATTGGGT TTT/gapGTGACT GTTGATATAGTG ACGACCT | T | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |
| 210 | cg43922383 | 250 | ATTGCCATTGG GTTTGTGACTGT TG/A/GJTATAGT GACGACCTCAG GAGCAACA | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |
| 211 | cg43922383 | 263 | TTGTGACTGTTG ATATAGTGACGA C[C/G]TCAGGAG CAACAGGTGGG TTAAAAA | C | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa. | 7.3E-185 | 2 |
| 212 | cg43953935 | 458 | CTTTTAAATAA ATGACTGCCGAG TG/A/GJGTGTA ATTCTGAGAAAA TTACATT | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD41634 LYOSOMAL TRAFFICKING REGULATOR 2 - MUS MUSCULUS (MOUSE), 703 aa (fragment). | 2.4E-177 | 13 |
| 213 | cg43933591 | 1167 | ACATTTTGAATT TTAGCTTTTTTTT [T/gap]GCCCTCTC TACTGTGTCACT AAATAT | T | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa. | 1.70E-176 | 8 |
| 214 | cg43949875 | 2329 | CTGAGTAGCTG GGATTACAGGC GTG[T/C]GCCAC CATGCCCCAGCT AATTTTTTG | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34394 NUCLEAR PORE COMPLEX INTERACTING PROTEIN NPIP - HOMO SAPIENS (HUMAN), 350 aa. | 6.60E-175 | |
| 215 | cg43100840 | 1131 | GGACAGGGGTG CAGCTGGCAGC CGA[G/A]AAAGG GGACCACCTCG GAGGGCTGG | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P49752 HYPOTHETICAL PROTEIN ZAP113 - Homo sapiens (Human), 309 aa (fragment). | 3.20E-168 | |

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|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|---|-----------|----|
| 216 | cg43922270 | 2077 | TGTATATGTGTA CGTAGGTAGAT GT[G/A]TGCAGC ATCGGCAGGT TTGCCAGG | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa. | 1.30E-162 | 2 |
| 217 | cg43993462 | 1461 | CAGAATGAGCT GCAGAGGTTTC CTC[C/T]CTGCTT TACAATCCCTTA TTGAAGT | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment). | 5.10E-161 | 5 |
| 218 | cg43993462 | 384 | TAAACATCTACA GAGTTGAAACAT A[A/C]TCTGTCAT ATTAAATATATT ATCTA | A | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment). | 5.1E-161 | 5 |
| 219 | cg43993462 | 624 | TAGTCTCACTTC TTACCAAAAAA A[A/gap]CAATGA ACTGGATTGAG CCCACTCA | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment). | 5.1E-161 | 5 |
| 220 | cg43329741 | 996 | GCAGTGCAGGA GATGACAGAGT GAG[G/A]AGGGC CCAGAGCAGAA TTCTGGCCC | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD3906 FH1/FH2 DOMAIN- CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa. | 6.7E-159 | |
| 221 | cg42910688 | 1687 | AAACAATTTTG TTCAATGCCCCAC C[G/A]AGACATA TAGAATTGGGAA CTGATA | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P55040 GTP-BINDING PROTEIN GEM (GTP-BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa. | 7.7E-158 | 8 |
| 222 | cg43967474 | 969 | TGCTGGGGACC ATGGATGGGGA GGA[G/gap]GGG CACAGGGCCCA GTGCAGATGAA | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA76848 KIAA1004 PROTEIN - HOMO SAPIENS (HUMAN), 496 aa (fragment). | 1.70E-152 | 11 |

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|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|---|-----------|---|
| 223 | cg43964140 | 160 | GCTGAGATCTTA GGTCAAAAAGC TAIC/TJAGAAA GAAATCACTTGG AAAAACA | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAC69899 SACM21 - MUS MUSCULUS (MOUSE), 721 aa. | 1.10E-150 | 6 |
| 224 | cg43990820 | 325 | CCGGTTTAAAG GAAAAGTAAAA AIC/AJAATCCAC AGTTGAGCAGTT GATGTG | C | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 3.30E-150 | 3 |
| 225 | cg43930377 | 682 | TCACAGCTGGA TTGAAAGAGTAT TT[G/A]GGAAT GTGGCAATGTT GTTTATAT | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 7.80E-149 | 4 |
| 226 | cg43969800 | 503 | GCAAGACGTGT CAGGGGAACCA AGG[C/T]TCAGA TCATTCCCCCTT CATCTACA | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P25686 DNAJ PROTEIN HOMOLOG 1 (HSJ-1) - Homo sapiens (Human), 351 aa. | 1.20E-145 | 2 |
| 227 | cg43973724 | 2109 | TATAAGTGTATG CAATAGAAATTT G[G/T]ATTTTGT ATAGAAAATTTA CCTTG | G | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75070 KIAA0483 PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment). | 1.30E-141 | 1 |
| 228 | cg43258867 | 112 | GGCCCAGTCCT GGGGCTCTGGG AGG[C/gap]TCAC GCTCCCTCCTC AGGCTGGGGA | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99773 HYPOTHETICAL 30.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 285 aa. | 2.60E-141 | |
| 229 | cg42907867 | 792 | GACGATGTGGA CGCTGGGAGGG ATC[T/gap]TGGC GTTGGTTTCTG AAAGCCAGG | T | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99769 HYPOTHETICAL 26.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 255 aa. | 1.10E-140 | 1 |

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|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|---|-----------|---------------------|
| 230 | cg43920176 | 2819 | AAAGCTGCTTTG TTAGGTTCCCTTA T[G/T]TTTTATTA ACTGTCITTTTCT CAGTT | G | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD28325 LUMAN2 - HOMO SAPIENS (HUMAN), 272 aa. | 1.40E-140 | |
| 231 | cg43920176 | 2909 | ATTTTGTCATTT TTTACATCAACT T[C/T]ATGGTCTT GTTTTACATGG TAATT | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD28325 LUMAN2 - HOMO SAPIENS (HUMAN), 272 aa. | 1.40E-140 | |
| 232 | cg43950100 | 856 | CAAAATTAAACA ATTCACAAAATA C[A/G]ACAGCTA GAATTACAAAAT CCATTC | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa. | 1.70E-139 | 11 |
| 233 | cg43950100 | 952 | GGCACAGGGAG AAAAACAAAGTG TT[C/gap]CAATC AGTCCAGGCAC AGGGACTGG | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa. | 1.70E-139 | 11 |
| 234 | cg43950100 | 391 | ACATTGACCCCT TCAGTTCCTATA T[G/A]CAGCACCC CAATATTCTTT GAAATA | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa. | 1.70E-139 | 11 |
| 235 | cg43950100 | 515 | CAGGTTTAGTGT TGTTGTAGTGG CA[C/T]TTGTCCA GAATTGGTACCT CCCCAT | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa. | 1.70E-139 | 11 |
| 236 | cg43132640 | 1317 | CTCTATGAACTC TGTTTCTTTTCT A[A/gap]TGAGAT ATTAAACCATGT AAAGAAC | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P11226 MANNOSE-BINDING PROTEIN C PRECURSOR (MBP-C) (MBP1) (MANNAN-BINDING PROTEIN) (MANNOSE-BINDING LECTIN) - Homo sapiens (Human), 248 aa. | 4.20E-134 | 10 (10q11.2) |

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|-----|------------|------|--|---|-----|--|--|--|----------------------|------------------|--|-----------|----|
| 237 | cg44938448 | 1310 | TGAAAGTTAGAGT AGCTGCAAATCT CT[<i>gap</i>]TAAGTA TCAATGTAAAGA AGCAGAT | T | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.80E-129 | 1 |
| 238 | cg44938448 | 511 | AATGCCACTTTC AGATGGAAGGG AA[<i>gap</i>]TGAGAT GGAAACAACA AAAAAGGA | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa. | 4.80E-129 | 1 |
| 239 | cg43949897 | 923 | AGCACTTTGGA GCTGGCCTCGC CCC[C/ <i>gap</i>]TAGG AGGAGAGGGTC CCTCCTGGGT | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O60499 SYNTAXIN 10 - HOMO SAPIENS (HUMAN), 249 aa. | 1.80E-126 | 19 |
| 240 | cg42549778 | 1067 | GGGGGTGCTCC TGGAAGCCCCA AGA[G/C]CATCC AGGATTGCCTC CCAGCTGCC | G | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD29690 PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1 - MUS MUSCULUS (MOUSE), 267 aa. | 3.70E-126 | |
| 241 | cg44028574 | 990 | CAGTCCCAGC TACCATGATGAG CC[C/ <i>gap</i>]TGGC GGCTTGAGCAC AGTGAGTGCT | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI- 15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa. | 4.00E-122 | 20 |
| 242 | cg44035718 | 1088 | TCTCATCTAGTG CTGAAGTCTGA GG[G/A]CTCTGC AGCATCAGACC CACCTCTA | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA83010 KIAA1058 PROTEIN - HOMO SAPIENS (HUMAN), 1534 aa (fragment). | 2.20E-121 | 2 |

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|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|--|-----------|----|
| 250 | cg42697161 | 552 | ACGTGGTGTGCTG GTAGTGTCTTGT TG[AG]GTGTGA ATTCTCTCTCAT ACAAAAG | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O15262 RING FINGER PROTEIN - HOMO SAPIENS (HUMAN), 247 aa. | 1.00E-114 | 4 |
| 251 | cg43957889 | 1466 | GTGCAATGGCA TGATCTCGGCT CAC[C/T]GCAAC CTGTGCCTCCC GGGTTCAAG | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa. | 2.70E-111 | 12 |
| 252 | cg42397024 | 404 | AACGTCAGACA AATTTTCAAAT CA[C/A]TCTTTA CTTCTCCAAGAT CTTCGA | C | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:O43583 DRP1 PROTEIN (DRP) - Homo sapiens (Human), 243 aa. | 4.30E-109 | |
| 253 | cg43976566 | 711 | CTTTAATGAAAC ACTTTGGATCGT C[A/G]GTGCTGA AGTGAAAAGAAT GTGCTG | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA74894 KIAA0871 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa. | 1.70E-107 | 4 |
| 254 | cg44001900 | 936 | GATGCTAAAAG CTTCTGCGAAAT GT[G/A]TTCACG TTTAATGTTGGG AAATCCC | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA83057 KIAA1105 PROTEIN - HOMO SAPIENS (HUMAN), 730 aa (fragment). | 1.20E-104 | |
| 255 | cg43954569 | 471 | TTCAGCCCACAT GACTCAGGGAC AC[A/gap]CTCCC CAGCGGTTGCT GGAGGCACC | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:P78560 DEATH DOMAIN CONTAINING PROTEIN CRADD (CASPASE AND RIP ADAPTATOR WITH DEATH DOMAIN) (RIP ASSOCIATED PROTEIN WITH A DEATH DOMAIN) - Homo sapiens (Human), 199 aa. | 1.40E-101 | 12 |
| 256 | cg43925519 | 791 | AGTGGCCCCCTT TCCCGCCCTGA AGA[T/C]GTTTCA CACGAAAAGGC CGTTTGTT | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P78317 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 190 aa. | 4.40E-100 | 4 |

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| 257 | cg43145684 | 711 | TGGCAAACTG CCAGCAGCGGT TGC[CT]GAAAA TGCTGGGTTGG GTGCCTACT | C | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA81668 DNA POLYMERASE ETA - HOMO SAPIENS (HUMAN), 713 aa. | 2.90E-99 | |
| 258 | cg43981803 | 626 | ACCAGCTCGGA GAGGGCACTTG AGA[G/T]GGTCT ATGAACAAATCT GTCTAAAA | G | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q16635 TFAZZIN - Homo sapiens (Human), 292 aa. | 7.1E-97 | X |
| 259 | cg44006111 | 1906 | AGGCCTGATGC ACATGTGCACA GGT[A/G]CCTAC ATGCTCTGTTCT TGTCACA | A | G | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to REMTREMBL- ACC:G1100182 T-CELL RECEPTOR BETA - HOMO SAPIENS (HUMAN), 311 aa. | 3.8E-95 | |
| 260 | cg44924968 | 1363 | TGGCCAGGGAC CTGAGCCCCGAG ACA[C/T]CCCTG CATTGATCCAA CCAGGTCA | C | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.8E-95 | 7 |
| 261 | cg44924968 | 1364 | GGCCAGGGACC TGAGCCCCGAGA CAC[C/T]CCTGC ATTGATCCCAAC CAGGTCAG | C | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment). | 6.80E-95 | 7 |
| 262 | cg43977021 | 1080 | TGTCATCTAAAG TAATTCATTAAAT GT[A]ACAGGAG TAGATGAGGCC TGGCACA | T | A | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |
| 263 | cg43977021 | 1087 | TAAAGTAATTCA TTAATGTACAGG A[G/A]TAGATGA GGCCTGGCACA CATAGCA | G | A | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |

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|-----|------------|------|--|---|---|--|--|--|----------------------|------------------|---|----------|---|
| 264 | cg43977021 | 1098 | ATTAATGTACAG GAGTAGATGAG GC[C]/TJGGCAC ACATAGCAGAA GGTAATGG | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |
| 265 | cg43977021 | 1107 | CAGGAGTAGAT GAGGCCTGGCA CAC[A]/GJTAGCA GAAGGTAATGG TTCTATAGG | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |
| 266 | cg43977021 | 1116 | ATGAGGCCTGG CACACATAGCA GAA[G]/AJGTAAT GGTCTATAGGT GTATCTTC | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |
| 267 | cg43977021 | 1169 | TAATGCACCTTG GGCTAGAGAAA TA[G]/CJAAAAATC ACACGTAACAAA AACAAA | G | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa. | 9.20E-91 | 6 |
| 268 | cg43999373 | 303 | CACAGAATTCAG AACTTTTTCACC C[G]/CJGAACTGG AGAAGGAGCAC TCCGTCA | G | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88994 HYPOTHETICAL 38.2 KD PROTEIN - RATTUS NORVEGICUS (RAT), 338 aa. | 1.50E-89 | 1 |
| 269 | cg43980889 | 915 | TTTGAGAGCTG CAGCAGAAAGCG GCT[G]/TJATCA CAGACTGGATTT AGTTATGA | G | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.5E-89 | |
| 270 | cg43980889 | 936 | GGCTGTATCAC AGACTGGATTTA GTT[G]/JATGATG AAAATACTGGAC TGTATTT | T | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.5E-89 | |

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| 271 | cg44030196 | 611 | TAGATTGTTTCAG TACTCAGCTCAC C/A/gap]CCCAT AGACCATTTCTC CTCTGGC | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD40853 SIRTUIN TYPE 5 - HOMO SAPIENS (HUMAN), 310 aa. | 7.4E-89 | |
| 272 | cg40336929 | 317 | GGCAACAAGTT ACAGCGGCGGG AGAAT/A]GTTCTT TCTCTCACCTGC CGGGGGG | T | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O73884 PUTATIVE PHOSPHATASE - GALLUS GALLUS (CHICKEN), 268 aa. | 3.4E-84 | |
| 273 | cg43920571 | 684 | AGAAGACAGCG CGCAGAAATAG TGC[G/A]GAGAG AAATGACCAGTA CTATTTAT | G | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P34624 HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III - Caenorhabditis elegans, 548 aa. | 3.5E-82 | 10 |
| 274 | cg43958980 | 537 | TAAGATCCTCCA TCCCACCAAAAA T[A/G]ACCCACA ATGACTCCAAAT CTTGTT | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43239 HYPOTHETICAL 41.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 383 aa (fragment). | 4.50E-82 | 6 |
| 275 | cg43320682 | 512 | CATTGGCAACG GCTGCCCACTA GGG[G/gap]CAC TGCCACTTGCCT GGCTCAAACT | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment). | 6.60E-81 | |
| 276 | cg42708544 | 845 | CCAGGCTTGCC TCTAGATTGGCT GG[G/gap]CCAG AATTTCTGGGGT CAGTCTGAA | G | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa. | 2.60E-79 | |
| 277 | cg43949796 | 637 | GGGAAGTAAAA TGAAGGAAGCA GAC[C/T]TCTTG CTCATCTTTCCA AATGAAAT | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q94547 RGA AND ATU GENES, COMPLETE CDS - DROSOPHILA MELANOGASTER (FRUIT FLY), 579 aa. | 1.20E-75 | 12 |

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| 278 | cg43298234 | 843 | TAAGGCCAGAG CTTGTTGCTG GGC[A/gap]CAGA AATCACCTGCTG CATCCTGTG | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa. | 1.30E-75 | 7 |
| 279 | cg43926358 | 607 | CAGTGATGTGC TGGCCCTTTCA GGG[A/C]CACAG GCCCTTCAGC TTCACCGGA | A | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75272 R33729_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 152 aa (fragment). | 1.90E-74 | 19 |
| 280 | cg35060315 | 1328 | CCAAACTATCTC ACCTACCCCTC CC[T/C]AGGATC CACTCTTTTGA ATGACAA | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa. | 9.50E-73 | 11 |
| 281 | cg35060315 | 1540 | CTATTTTATCCA TCCATGTTCTCC C[A/gap]AATCTG TGCTTTCTTTCA ACAGGTT | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa. | 9.50E-73 | 11 |
| 282 | cg35060315 | 1542 | TTTATCCATCC ATGTTCTCCCAA A[gap]/A/TCTGTG CTTCTTTTCAAC AGGTTAT | gap | A | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa. | 9.5E-73 | 11 |
| 283 | cg35060315 | 1557 | GTTCCTCCAAAT CTGTGCTTTCTT T[C/T]AACAGGTT ATATATTAAAC TATTT | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa. | 9.5E-73 | 11 |
| 284 | cg35060315 | 1562 | CCCAAATCTGTG CTTCTTTTCAAC A[G/C]GTTATATA TTAAAACTATTT CATGA | G | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa. | 9.5E-73 | 11 |

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|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|--|---------|----|
| 285 | cg44126579 | 18 | TGTACAACTGAT TAGAG[AGap]GT TTTTTTTTCTTT TTCTTTTCAA | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa. | 1.1E-71 | 16 |
| 286 | cg43951096 | 719 | CCTCTCCTCCAA GAGTTGGTTCC GC[AGap]AGAG GTGGAAGAAC TCTCAATAGT | A | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2E-71 | 17 |
| 287 | cg43951096 | 884 | CACAGCCATAAT ATAGAGAACAG AG[C/gap]TTCTC CATGAACATCCA CCAGGCTG | C | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2E-71 | 17 |
| 288 | cg43960676 | 65 | AGCAGCCAGCT TCATTGGCTGCA AA[C/T]GCCTCT CTCAGGTGAGT CAAAGGAG | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD43443 26S PROTEASOME SUBUNIT P40.5 - MUS MUSCULUS (MOUSE), 376 aa. | 5.3E-69 | |
| 289 | cg43323149 | 1101 | TCACCTCAGATG AGTGTGGCTCC CC[C/G]CGCTCC CATACTGCAGC CTGCCCCCT | C | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa. | 1E-68 | 1 |
| 290 | cg43969533 | 364 | AAGGGAAGCCT ATCCTATTTTTT TT[AGap]TCCTTT GCGAAAACAGAG AGCCAAGT | T | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa. | 1.6E-67 | 7 |
| 291 | cg43969533 | 365 | AGGGAAGCCTA TCCTATTTTTTT TT[AGap]CCCTTG CGAAAACAGAA GCCAAGTT | T | gap | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa. | 1.6E-67 | 7 |

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|-----|------------|-----|--|---|---|--|--|--|----------------------|------------------|--|---------|----|
| 292 | cg39376027 | 601 | CCGGGGAGGTG GTTCTGGTAATC TG[GT]GGGGA GCCGGGACAGG CGCCCCGA | G | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD39515 HERMES - MUS MUSCULUS (MOUSE), 197 aa. | 2.3E-66 | |
| 293 | cg39376027 | 604 | GGGAGGTGGTT CTGTAATCTG GG[G/TT]GGAGC CGGACACGGCG CCCCGAGTT | G | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD39515 HERMES - MUS MUSCULUS (MOUSE), 197 aa. | 2.3E-66 | |
| 294 | cg43976681 | 210 | CTCTCTCTTCGC CGCCGACGCAG AA[A/G]GGAGCT GGGAGGAAAA AGCTGCTG | A | G | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD29427 MYOMEGALIN - RATTUS NORVEGICUS (RAT), 2324 aa. | 4.3E-66 | 11 |
| 295 | cg43085556 | 131 | GTAAGGTAAAT GTGAATCAATAT G[T/C]TAGTTCT GGCAATTATTC TGCAAA | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa. | 8.8E-65 | |
| 296 | cg43085556 | 149 | CAATATGTTAGT TCTGGGCAATTA TT[T/C]CTGCAAT TCTGCCAGATAA TTAAA | T | C | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa. | 8.8E-65 | |
| 297 | cg43085556 | 150 | AATATGTTAGTT CTGGGCAATTAT T[C/TT]TGCAAAAT CTGCCAGATAAT TAAAG | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa. | 8.8E-65 | |
| 298 | cg43085556 | 30 | TTGTTGTTCTCA AGCTTTTCGCCT A[C/TT]ATTTAGA CTAACCCCTGCTT ATTCC | C | T | | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa. | 8.8E-65 | |

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|-----|------------|------|--|-----|-----|--|--|----------------------|------------------|---|---------|----|
| 299 | cg43085556 | 45 | TTTTGCCTACA TTTTAGACTAAC C[C/T]TGCCTATT CCTGTGAATCAA GTGGT | C | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa. | 8.8E-65 | |
| 300 | cg43085556 | 65 | TAACCCCTGCTTA TTCCTGTGAATC A[A/C]GTGGTGA TCTTCTGCAGCT TGAAT | A | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa. | 8.8E-65 | |
| 301 | cg43920089 | 437 | GCATTTGCTGCT TGTGCTTGATTT T[G/A]TTTGGCT CAATCCCTTCCT GGCAGC | G | A | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14716 DNAJ PROTEIN - HOMO SAPIENS (HUMAN), 135 aa. | 2E-63 | |
| 302 | cg43950850 | 263 | AAACATGTTCCA TCAAAATTCAGAA A[C/gap]AGCAGG TATCAGTGAAAC TGGAGCA | C | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa. | 7.8E-62 | 11 |
| 303 | cg43950850 | 736 | AGGAAAACCCAC GACGACCACTA CCC[G/C]GGCCT AAGCGGTCAGC TTTCTCCTC | G | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa. | 7.8E-62 | 11 |
| 304 | cg44128084 | 1012 | CATCCGCGCTG ACGGCAGTCAC CGG[T/C]GAGAC CGGCGCCGGAA AGACCATGG | T | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.7E-59 | |
| 305 | cg43976473 | 984 | GACGCTCGCTG TCCCCGAGGGC CCG[gap/C]TGC GCCGCCCTCGTG GGTACGAATAC | gap | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa. | 3.5E-59 | 11 |

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|-----|------------|-----|--|---|---|--|--|----------------------|------------------|--|----------|----|
| 306 | cg44924858 | 546 | GCTTCTGTCAGAG CGTTACTTTTCAC C[G]AJTGCCTGC TGTTCCACAGG AAGAGT | G | A | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa. | 4.3E-59 | |
| 307 | cg44924858 | 558 | CGTTACTTTTCAC CGTGCCTGCTG TTT[C]CCACAG GAAGAGTCTGT CTGTTCCA | T | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa. | 4.3E-59 | |
| 308 | cg44924858 | 755 | ACCCAGCTTG CCCGGCAGCAC ACA[A]GJAACGT TTTCTTTGGCTT GACGAATA | A | G | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa. | 4.30E-59 | |
| 309 | cg43961591 | 222 | ACACCACTGGT ACTCACACCCC CTC[T/C]GGCTG GGTCTCTGGT GGGCCCTGC | T | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:O35414 STATHMIN-LIKE PROTEIN B3 (RB3) - Rattus norvegicus (Rat), 189 aa. | 3.10E-58 | |
| 310 | cg43924285 | 528 | CTGCATATGTTT GCAGTTTTCAT C[A/G]ACTTCTTC ATAAACAAACAA ACATT | A | G | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa. | 4.20E-57 | 15 |
| 311 | cg43924285 | 574 | ACATTTTCTAGA AACCAAAATATG T[A/G]GTGGCCC AAAGGAGCTCTT AAGCAA | A | G | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa. | 4.20E-57 | 15 |
| 312 | cg43958224 | 198 | GTTTGATCCTCA GCCAGGACGCA CA[G/A]GCCCTA CAAGATCCCG CCCTCCAA | G | A | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment). | 2.30E-53 | 19 |

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|-----|------------|-----|--|---|-----|--|--|----------------------|------------------|---|----------|--|
| 313 | cg43971060 | 502 | AACGGCTTTAAA CACAAAGCTCAG GG[G]gapICTTG GGGTTTATCCC GAGGGCACAG | G | gap | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P31639 SODIUM/GLUCOSE COTRANSPORTER 2 (NA(+)/GLUCOSE COTRANSPORTER 2) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 672 aa. | 4.20E-53 | |
| 314 | cg44927952 | 342 | TATTTTTCATTG TACTTATTATTC A[T/C]TATACTTA CTATATATATTT AAAAAC | T | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD34077 CGI- 82 PROTEIN - HOMO SAPIENS (HUMAN), 318 aa. | 4.80E-52 | |
| 315 | cg19885484 | 77 | AAACAACAAAT AACCACAAATAA A[C/T]CAACTAAT GCTACACAGAAT GTGAT | C | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15019 KIAA0301 - HOMO SAPIENS (HUMAN), 2047 aa (fragment). | 1.90E-51 | |
| 316 | cg42307356 | 11 | CGGCCGCGG[C] G/TJCGGAACGG CGCCTCCCGCC CCACCA | G | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15121 PUTATIVE FATTY ACID DESATURASE MLD - HOMO SAPIENS (HUMAN), 323 aa. | 2.60E-51 | |
| 317 | cg44005017 | 947 | TGGGAGGCCTG GTTGCCCTCC CGG[C/T]GTGCT GGGACACTCTG GGTTCCTGC | C | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43363 HYPOTHETICAL 23.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 204 aa. | 5.00E-51 | |
| 318 | cg43329819 | 609 | TTGAGCTCTCCT ACAAGCTGGAG GC[A/C]AACAGT CAGTGAGAGCG GGGGGGCC | A | C | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa. | 1.40E-50 | |
| 319 | cg43329819 | 612 | AGCTCTCTCTACA AGCTGGAGGCA AA[C/T]AGTCAG TGAGAGCGGG GGGCCAGT | C | T | | | SILENT- NONCODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa. | 1.40E-50 | |

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|-----|------------|------|---|---|---|-----|-----|-------------------|---------------------------|---|-----------|----|
| 326 | cg43930957 | 1287 | AAATATAAACTC TTTTGAAAGTTG T[G]GGTCAGC TGACCAGGTAG AGGATTC | G | T | Val | Val | SILENT- CODING | apoptosi s | Human Gene Homologous to SPTREMBL-ID:Q62627 CLONE PAR- 4 INDUCED BY EFFECTORS OF APOPTOSIS - RATTUS NORVEGICUS (RAT), 332 aa. | 1.6E-117 | |
| 327 | cg43300636 | 413 | CAAGGCGGCA AAGATGGGAC CAG[C]TACCAC AGCGCCACGC CCACCTCCG | C | T | Val | Val | SILENT- CODING | ATPase_ associat ed | Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H+)-TRANSPORTING ATP SYNTHASE) (H+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa. | 1.7E-175 | |
| 328 | cg43967912 | 749 | CATTCTCTCTCC AAAATTTCTCAG A[T]CJTGTGCA CAGGACTCCATT CCAACC | T | C | Lys | Lys | SILENT- CODING | ATPase_ associat ed | Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREBISIAE VACUOLAR H(+)- ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa. | 5.6E-108 | 8 |
| 329 | cg43967912 | 761 | AAATTTCTCAG ATTTGTGCACAG G[A]GJCTCCATT CCAACCTTCCA GATTTAA | A | G | Ser | Ser | SILENT- CODING | ATPase_ associat ed | Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREBISIAE VACUOLAR H(+)- ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa. | 5.60E-108 | 8 |
| 330 | cg43967912 | 773 | ATTTGTGCACAG GACTCCATTCCA A[C]TJCTTCCAG ATTTAAGTTCTG AACTGT | C | T | Arg | Arg | SILENT- CODING | ATPase_ associat ed | Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREBISIAE VACUOLAR H(+)- ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa. | 5.60E-108 | 8 |
| 331 | cg43132502 | 371 | AGTGGGTGGCA CCGCCGAGGCT GCT[G/A]TTACG GCTCATCTTCAT TGATTTCG | G | A | Leu | Leu | SILENT- CODING | ATPase_ associat ed | Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa. | 9.40E-58 | 11 |

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|-----|------------|------|---|---|---|-----|-----|-------------------|---------------|---|-----------|---------------|
| 332 | cg44924856 | 352 | ACACGCCAGC AGCCGAATGAT GTTT/GJGGGTC CTTGAGCCTCG ACATGATCT | T | G | Pro | Pro | SILENT- CODING | cadherin | Human Gene Similar to SWISSPROT- ID:Q08345 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (TRK E) (PROTEIN- TYROSINE KINASE RTK 6) - HOMO SAPIENS (HUMAN), 913 aa. | 7.90E-77 | 6 (6q16) |
| 333 | cg43991318 | 2634 | AGCACTCCCT GGCTCACCTT CTCT/CJCCTCG TGGTCCCTTTTC ACCTGGTG | T | C | Ser | Ser | SILENT- CODING | collagen | Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa. | 1.30E-73 | 1 (1p34) |
| 334 | cg41553795 | 480 | CTGTGCACGTG GTTGTCGCTGA GAC[C/T]GACTA CCAGAGTTTCG CTGTCCTGT | C | T | Thr | Thr | SILENT- CODING | complement | Human Gene Homologous to SWISSPROT-ID:P07360 COMPLEMENT C8 GAMMA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 202 aa. | 1.40E-104 | 9 (9q34.3) |
| 335 | cg43973728 | 286 | GCAAAATTCAGAT GCAAGCCGTG GC[C/T]AACGGG AAGGTTCTTCCG AATGATC | C | T | Ala | Ala | SILENT- CODING | cyclin | Human Gene SWISSPROT- ID:P51946 CYCLIN H (MO15- ASSOCIATED PROTEIN) (P37) (P34) - HOMO SAPIENS (HUMAN), 323 aa. | 2.60E-172 | 5 (5q13.3) |
| 336 | cg43312829 | 1413 | TCCAATCAAAGA CAACAGGACTC CAIT/CIGTAACT GAATATGAGGA CAATTGTA | T | C | His | His | SILENT- CODING | dehydrogenase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa. | 0.00E+00 | 4 |

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|-----|------------|------|--|---|---|-----|-------------------|-------------------|---|----------|---|
| 337 | cg43312829 | 1422 | AGACAAACAGGA CTCCATGTAAC GATGATGAG GACAAATTTGAAG AAATCAT | A | G | Glu | SILENT- CODING | dehydrog enase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |
| 338 | cg43312829 | 1452 | AGGACAAATTTGA AGAAATCATGG GTATGTTGAAA GAGCTATATTCT GTTAGAA | A | G | Val | SILENT- CODING | dehydrog enase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |
| 339 | cg43312829 | 1473 | GGGTATGGAAA GAGCTATATTCT GTTCJAGAAATA TAAGGCCATCCT GCCACG | T | C | Val | SILENT- CODING | dehydrog enase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |

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|-----|------------|------|--|---|---|-----|-----|-------------------|-------------------|---|-----------|----|
| 340 | cg43312829 | 1569 | ACTGGATATTGA GAGGAATGGAG CC[G/A]TGGACT CTAAACATAAA GGCTCTG | G | A | Pro | Pro | SILENT- CODING | dehydrog enase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa. | 0.00E+00 | 4 |
| 341 | cg43312829 | 1623 | TGAACGGCTC AAGCCAGCCAA GGA[T/C]TGAC ACCCATTGAGTA TCCAAAC | T | C | Asp | Asp | SILENT- CODING | dehydrog enase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa. | 0.00E+00 | 4 |
| 342 | cg43307992 | 652 | TCGAGGGCCCC AACTTTGAGTTC TC[C/A]ACGGAG ACCCATGAGGA GCTGCTGT | C | A | Ser | Ser | SILENT- CODING | dehydrog enase | Human Gene Homologous to SPTREMBL-ID:O00217 MITOCHONDRIAL NADH DEHYDROGENASE-UBIQUINONE FE-S PROTEIN 8, 23 KDA SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 210 aa. | 1.70E-113 | 11 |
| 343 | cg43969759 | 965 | TGGCTGTGGGC TTCACCCAGCCTC AC[C/T]ACCTCC TCCAGGGAGTT GACTTCAG | C | T | Val | Val | SILENT- CODING | dehydrog enase | Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa. | 1.80E-109 | 11 |

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|-----|------------|-----|---|---|---|-----|-----|-------------------|-------------------|--|----------|--|
| 344 | cg39523614 | 318 | ATGCTGGATCA GATCCAGCTGC ACTATTAAGTGT CGAGCCGACGA AGATGGGG | A | T | Leu | Leu | SILENT- CODING | dehydrog enase | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa. | 2.10E-76 | |
| 345 | cg39523614 | 360 | AAGATGGGGAC AGTTTCGTCCTG AA[C/T]GGCGTC AAGGCTTGGGT CACGGAGG | C | T | Asn | Asn | SILENT- CODING | dehydrog enase | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa. | 2.10E-76 | |
| 346 | cg39523614 | 366 | GGGACAGTTTC GTCCTGAACGG CGT[C/T]AAGGC TTGGGTCACGG AGGCTGGCG | C | T | Val | Val | SILENT- CODING | dehydrog enase | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa. | 2.10E-76 | |
| 347 | cg39523614 | 613 | TCAGGGGCACG GTCTGAGTGTT GCTT[C/T]GGGT ACGCTTGACAA CTCTCGTGT | T | C | Leu | Leu | SILENT- CODING | dehydrog enase | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa. | 2.10E-76 | |
| 348 | cg39523614 | 660 | GTGTCGATTGG CTGCTCAAGCA GT[G/A]GGAATT GCCCAGGGAGC TTTAGACA | G | A | Val | Val | SILENT- CODING | dehydrog enase | Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa. | 2.10E-76 | |
| 349 | cg42717491 | 207 | AGGCTCACACT CACTTCATGTTT TT[C/G]ACAAAG TCCTCGCCTTTC TTGATGG | C | G | Val | Val | SILENT- CODING | dehydrog enase | Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa. | 2.40E-52 | |

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|-----|------------|------|--|---|---|-----|-----|-------------------|-------------------|--|-----------|----|
| 350 | cg42717491 | 252 | TGATGGAGGCT TTCAGCTCAGG GAT[G/A]GCCTC GGCAATCATTTT CTCCTCAA | G | A | Ala | Ala | SILENT- CODING | dehydrog enase | Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa. | 2.40E-52 | |
| 351 | cg42717491 | 270 | CAGGGATGGCC TCGGCAATCATT TT[C/T]TCCTCAA AAGGAGTGATTT TGCCAA | C | T | Glu | Glu | SILENT- CODING | dehydrog enase | Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa. | 2.40E-52 | |
| 352 | cg42717491 | 288 | TCATTTTCTCCT CAAAAGGAGTG ATT[C/T]TGCCAA TGCCTAGGTTCT TCTCCA | T | C | Lys | Lys | SILENT- CODING | dehydrog enase | Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa. | 2.40E-52 | |
| 353 | cg42711596 | 1535 | ATTAGTATGCT GTGAGCTGCTT TT[G]GTTGAATC TGATTAGTTTC AGTTTC | T | G | Thr | Thr | SILENT- CODING | eph | Human Gene Homologous to SWISSPROT-ID:P48722 OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG- 1) - MUS MUSCULUS (MOUSE), 838 aa. | 2.10E-115 | 4 |
| 354 | cg43319420 | 1557 | AGAAAGTCAGAA GGCCTTCCTGT GGC[A/C]CCGTT CATGGACCGAG ACAAAGTGA | A | C | Ala | Ala | SILENT- CODING | esterase | Human Gene Similar to SWISSNEW- ID:Q23917 3':5'-CYCLIC- NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. pcis:SWISSPROT-ID:Q23917 3':5'- CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. | 3.30E-60 | 21 |

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|-----|------------|------|---|---|---|-----|-----|-------------------|--------------|--|-----------|----|
| 355 | cg41029366 | 687 | AGTGGGGATCA GTGTGCGATGA CAC[T/C]TGGGA CCTGGAGGACG CCCACGTGG | T | C | Thr | Thr | SILENT- CODING | glycoprotein | Human Gene SPTREMBL-ID:Q61003 T CELL SURFACE GLYCOPROTEIN CD6 - MUS MUSCULUS (MOUSE), 665 aa. | 1.00E-234 | 11 |
| 356 | cg42876034 | 860 | GCGCCCGCCGC GGCAGCGCCCC GAG[G/C]CCGGC TTCGGCCCGCA GCCTGGACG | G | C | Gly | Gly | SILENT- CODING | glycoprotein | Human Gene Similar to SWISSPROT- ID:Q07066 22 KD PEROXISOMAL MEMBRANE PROTEIN - RATTUS NORVEGICUS (RAT), 193 aa. | 2.60E-78 | |
| 357 | cg43976227 | 258 | CTGGTGTGATCT CTGTCTCTTTAT G[G/A]ACCACTA CTTTGGTCACTG ACATGT | G | A | Val | Val | SILENT- CODING | glycoprotein | Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 2.60E-60 | 18 |
| 358 | cg43916642 | 816 | GGCTGAAAAGC ATATCTATACAT TC[G/A]GAGAAG TCGCAAAATAGAA AGGAAA | G | A | Ser | Ser | SILENT- CODING | helicase | Human Gene Similar to SWISSPROT- ID:P25888 PUTATIVE ATP- DEPENDENT RNA HELICASE RHLE- ESCHERICHIA COLI, 454 aa. | 2.90E-54 | 1 |
| 359 | cg43925670 | 2320 | AACCAGCATCA CCTCGGAACCTT TC[T/C]TCCATCA AGTCAGCAATCT GAATTT | T | C | Glu | Glu | SILENT- CODING | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. lpcds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0.00E+00 | 1 |

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|-----|------------|------|--|---|---|-----|-----|-------------------|------------|--|----------|---|
| 360 | cg43925670 | 2370 | TTGTCATACCTCT TCTCTCATTTT AAGGATTAAGTT TTAAATCGTTGC TCAGT | A | G | Leu | Leu | SILENT- CODING | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcsls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0.00E+00 | 1 |
| 361 | cg43925670 | 2389 | TTTTAAATTAA GTTTAAATCGT T[G/A]CTCAGTA AGGACTTAACCA TTCTAA | G | A | Ser | Ser | SILENT- CODING | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcsls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0.00E+00 | 1 |
| 362 | cg43925670 | 2446 | AATCATTGATGA CCTCTAATCCTT TTT/CJAGTAGAA CAATGTTCTTGT ATTTT | T | C | Leu | Leu | SILENT- CODING | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcsls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0.00E+00 | 1 |

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|-----|------------|------|---|---|---|-----|-----|-------------------|-----------|--|-----------|---------------|
| 363 | cg44004587 | 1913 | TTTTATTGTCAT TTTCATCAATAA G[G/A]ATACACA TCTCTGCCAGG AGTIGAA | G | A | Ile | Ile | SILENT- CODING | isomerase | Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa. | 3.00E-123 | |
| 364 | cg43257400 | 2144 | CATGTGTGGTAA CTCCTCAAGATG G[G/C]GAGACGT TAGCACAAATGA TAGAAG | G | C | Gly | Gly | SILENT- CODING | kinase | Human Gene SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa. | 0.00E+00 | 10 |
| 365 | cg43931272 | 2072 | TTGGTGGTCTT TCCCAACCACAA A[A/G]CACTCCG GTGGTAAATACC AATAAG | A | G | Cys | Cys | SILENT- CODING | kinase | Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa. | 0.00E+00 | |
| 366 | cg42665067 | 748 | GGGCTTCTAC ATATCCCCCCG AAG[C/T]ACCTT CAGCACTCTGC AGGAGCTGG | C | T | Ser | Ser | SILENT- CODING | kinase | Human Gene SWISSPROT- ID:P08631 TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.12) (P59- HCK AND P60-HCK) (HEMOPOIETIC CELL KINASE) - HOMO SAPIENS (HUMAN), 526 aa. | 9.20E-289 | 20 (20q11) |
| 367 | cg43982923 | 634 | CGATGCAGAAA TACGAGAAACT GGA[A/G]AAGAT TGGGGAAGGCA CCTACGGAA | A | G | Glu | Glu | SILENT- CODING | kinase | Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa. | 3.60E-159 | 19 |
| 368 | cg43982923 | 655 | TGGAAGAAGATTG GGGAAGGCACC TA[C/T]GGAAC GTGTTCAAGGC CAAAAACC | C | T | Tyr | Tyr | SILENT- CODING | kinase | Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa. | 3.60E-159 | 19 |

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|-----|------------|-----|---|---|---|-----|-----|-------------------|---------------------|--|-----------|----|
| 369 | cg43982923 | 697 | CCAAAACCGG GAGACTCATGA GATC/TGTGGC TCTGAAACGGG TGAGGCTGG | C | T | Ile | Ile | SILENT- CODING | kinase | Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa. | 3.60E-159 | 19 |
| 370 | cg43919086 | 576 | CGCTCAGGAGG ATATAGGTGATG AC/A/GCCGATG CTCCACATGTCC GCCTCCA | A | G | Gly | Gly | SILENT- CODING | kinase | Human Gene TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 6.80E-158 | 19 |
| 371 | cg25143358 | 407 | GGCGGCTTCA AGTTTCGTGGTC AT[G/A]CCGCCG GTTCCACACCC CGAACCCAG | G | A | Gly | Gly | SILENT- CODING | kinase | Human Gene Similar to SWISSPROT- ID:P46546 GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) - CORYNEBACTERIUM GLUTAMICUM, 369 aa. | 2.70E-51 | |
| 372 | cg43105476 | 514 | GGTCCGATGC CCCACATTGCT GGC[C/T]GTGTG CTTCACCAGGA ACTCCACCA | C | T | Thr | Thr | SILENT- CODING | kinasein hibitor | Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa. | 7.80E-86 | |
| 373 | cg43105476 | 541 | TGTGCTTCACCA GGAACCTCCACC AC[C/A]CGGAGG TGGCCTTCTTTG GCAGCCA | C | A | Arg | Arg | SILENT- CODING | kinasein hibitor | Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa. | 7.80E-86 | |
| 374 | cg43105476 | 595 | GCAAGGCGCAGG TTCCCTTCATTA TC[C/T]TCGATGT TAAACATCAGCTT GAAACT | C | T | Glu | Glu | SILENT- CODING | kinasein hibitor | Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa. | 7.80E-86 | |

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|-----|------------|-----|---|---|---|-----|-----|-------------------|---------------------|---|----------|---------------|
| 375 | cg43105476 | 616 | TATCCTCGATGT TAACATCAGCTT GTA/GAACTCCA GCAAAGTCTGTA AAGTGT | A | G | Phe | Phe | SILENT- CODING | kinasere hibitor | Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa. | 7.80E+06 | |
| 376 | cg43939695 | 410 | CAGGGAACAGC AATGGGAACGC CAGT/CJATCAA CATCACGGACA TCTCAAGGA | T | C | Ser | Ser | SILENT- CODING | kinasere ceptor | Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15 (15q25) |
| 377 | cg43939695 | 419 | GCAATGGGAAC GCCAGTATCAA CATC/TJACGGA CATCTCAAGGAA TATCACTT | C | T | Ile | Ile | SILENT- CODING | kinasere ceptor | Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15 (15q25) |
| 378 | cg43939695 | 467 | CTTCCATACACA TAGAGAACTGG CGC/AJAGTCTT CACACGCTCAA CGCCGTGG | C | A | Arg | Arg | SILENT- CODING | kinasere ceptor | Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15 (15q25) |
| 379 | cg43939695 | 473 | TACACATAGAGA ACTGGCGCAGT CTT/GJCACACG CTCAACGCCGT GGACATGG | T | G | Leu | Leu | SILENT- CODING | kinasere ceptor | Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15 (15q25) |
| 380 | cg43939695 | 479 | TAGAGAACTGG CGCAGTCTTCA CAC[G/A]CTCAA CGCCGTGGACA TGGAGCTCT | G | A | Thr | Thr | SILENT- CODING | kinasere ceptor | Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15 (15q25) |

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|-----|------------|------|---|---|---|-----|-----|-------------------|----------|---|-----------|---|
| 394 | cg44929972 | 1266 | ATGTCCTGAGG GCAGTGGAGGA ACG[A]GATTT TCCAACAGAAAC CATTAAAT | G | A | Arg | Arg | SILENT- CODING | ngf | Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa. | 4.70E-214 | 7 |
| 395 | cg44926604 | 1283 | AGTCGATGTCC AGCTTGCGGGC CACG[A]CGGTG TAGATTGGGCA GGTTCAGCT | G | A | Arg | Arg | SILENT- CODING | nuclease | Human Gene SWISSPROT- ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) - HOMO SAPIENS (HUMAN), 939 aa. | 0.00E+00 | 3 |
| 396 | cg38642684 | 282 | GCCAGTTAATAT TGCCTAGTAATT TTC/TGTGATAATC ATTTAAGGTATG TAAGT | C | T | Gln | Gln | SILENT- CODING | nuclease | Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |
| 397 | cg38642684 | 387 | AAGGATACTTCC AAGGAGAGGAC ATT/CJTGACTT TTTCAGGTGCAA TGATTA | T | C | Gln | Gln | SILENT- CODING | nuclease | Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |

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|-----|------------|------|---|---|---|-----|-----|-------------------|----------|---|----------|----------|
| 398 | cg38642684 | 405 | AGGACATTTGTA CTTTTCAGGTG C/A/TJATGATTAA ACCACTTAACTG TGCAT | A | T | Ile | Ile | SILENT- CODING | nuclease | Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |
| 399 | cg38642684 | 456 | TCCTTATGACAG AGGTATATAAAC TTT/CJAAAAGCA CTGGCTCCACT GGGGCTG | T | C | Leu | Leu | SILENT- CODING | nuclease | Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |
| 400 | cg43919677 | 2577 | TTGAAGTAGCTC CTGAAGCTTCTA C/G/AJTCTAGTG CCAGCCAAGTG ATTGCTC | G | A | Thr | Thr | SILENT- CODING | oncogene | Human Gene SWISSPROT- ID:Q00918 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1- BP- 1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT) - RATTUS NORVEGICUS (RAT), 1712 aa. | 0.00E+00 | 2 (2p12) |

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|-----|------------|------|--|---|---|-----|-----|-------------------|-----------------|---|-----------|---------------|
| 401 | cg44005163 | 1384 | CCTGTGGGCTG ATTACATTAAC GAT/CJGCACAA AGATTATGTAAT GCTTTAT | T | C | Asp | Asp | SILENT- CODING | oncogen e | Human Gene SWISSPROT- ID:P12756 SKI-RELATED ONCOGENE SNOA - HOMO SAPIENS (HUMAN), 415 aa. | 5.30E-229 | |
| 402 | cg44005163 | 1423 | GTAATGCTTTAT TGCGGCCACGA AC/T/GJTTCCTC AAATGGTAGC GTACTTC | T | G | Thr | Thr | SILENT- CODING | oncogen e | Human Gene SWISSPROT- ID:P12756 SKI-RELATED ONCOGENE SNOA - HOMO SAPIENS (HUMAN), 415 aa. | 5.30E-229 | |
| 403 | cg25334466 | 546 | TCAAGGACCCAG TTCACCTACCCCTC CC/T/CJGAGGTG AAGGACTGATG CTTTGCCA | T | C | Pro | Pro | SILENT- CODING | oxidase | Human Gene Homologous to SWISSPROT-ID:P25689 URICASE (EC 1.7.3.3) (URATE OXIDASE) - PAPIO HAMADRYAS (HAMADRYAS BABOON), 303 aa. | 1.30E-149 | |
| 404 | cg42535091 | 750 | AACTGAAATACGA ACGTTGGTGGA GG[A/G]GAACGG TTTGATTCTTTG ACAGATC | A | G | Gly | Gly | SILENT- CODING | phosphat ase | Human Gene SWISSPROT- ID:Q06124 PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (PTP-1D) (SH-PTP3) (SH- PTP2) - HOMO SAPIENS (HUMAN), 593 aa. | 0.00E+00 | 12 |
| 405 | cg43302847 | 1227 | GGTGGTGGTGG CCATCCAGATC CTG[C/A]GGAAG AACCCCAAAGG CTTCTCTT | C | A | Arg | Arg | SILENT- CODING | phosphat ase | Human Gene SWISSPROT- ID:P05186 ALKALINE PHOSPHATASE, TISSUE- NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP- TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa. | 3.20E-286 | 1 (1p36.1) |
| 406 | cg39728924 | 433 | GGCAAAATGGTG TTGGAAAATAAT TC[G/A]AATGTTA TTGCCATGATAA CCAGAG | G | A | Ser | Ser | SILENT- CODING | phosphat ase | Human Gene Similar to TREMBLINW-ID:D1024666 PROTEIN-TYROSINE- PHOSPHATASE (EC 3.1.3.48) - MUS MUSCULUS (MOUSE), 426 aa. | 1.20E-64 | |

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|-----|------------|------|---|---|---|-----|-----|-------------------|-------------------|---|-----------|---------------|
| 407 | cg42881873 | 1564 | ACCTGAAAGCG AGCGACTGGAA AGT[A/G]AACGG CGCGGTCATA AAGTTAGCC | A | G | Val | Val | SILENT- CODING | protease | Human Gene SWISSNEW-ID:P29122 SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-) - HOMO SAPIENS (HUMAN), 969 aa. pcls:SWISSPROT-ID:P29122 SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-) - HOMO SAPIENS (HUMAN), 969 aa. | 0.00E+00 | 15 (15q26) |
| 408 | cg42913398 | 589 | CTGTTCCGTGG ATGAGAAGATA GTC[T/C]ACATTT CTGAAATATTCT GCTCTTG | T | C | Val | Val | SILENT- CODING | protease | Human Gene SPTREMBL-ID:O00199 INTEGRAL MEMBRANE SERINE PROTEASE SEPRASE - HOMO SAPIENS (HUMAN), 760 aa. | 0.00E+00 | 2 |
| 409 | cg44028327 | 793 | TTCGAATTACCT ACTCAATTGTGC A[A/G]ACGAATT GTTCCAAAGAG AATTTTC | A | G | Gln | Gln | SILENT- CODING | protease nhib | Human Gene SWISSPROT- ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) - HOMO SAPIENS (HUMAN), 644 aa. | 0.00E+00 | 3 (3q27) |
| 410 | cg43979831 | 899 | CCTCAAGGACC ACTCCCAAGA CTT[C/T]TATGTT GATGAGAACAC AACAGTCC | C | T | Phe | Phe | SILENT- CODING | protease nhib | Human Gene SWISSPROT- ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa. | 1.10E-228 | 14 |
| 411 | cg43987538 | 905 | ATCATCATAAGA GAAGAATCATTT TTT[A/J]CCAGTAG CCCCACTACCAT GAATGA | T | A | Gly | Gly | SILENT- CODING | reductas e | Human Gene SWISSPROT- ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA- CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa. | 1.10E-171 | 1 (1p31) |
| 412 | cg42717608 | 142 | CCACAAAGGTC TATGTCCAGCAC CT[G/T]CTGAAG AGAGACAAAGA ACACCTGT | G | T | Leu | Leu | SILENT- CODING | reductas e | Human Gene Similar to SWISSNEW- ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa. pcls:SWISSPROT-ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa. | 1.80E-51 | |

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|-----|------------|------|--|---|---|-----|-----|-------------------|--------|---|-----------|-----------------|
| 413 | cg43927378 | 4726 | ATCTGATGGAG AACTACACAGATC GTT/CJGTCAGC AACCTGGCCAC TGAGCGTG | T | C | Val | Val | SILENT- CODING | struct | Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa. | 0 | 2 |
| 414 | cg43945592 | 1503 | GGGCTCGGGCA GGGTACACAAA CTC/T/CJGTGGC TGCAAAATCCCC AGAGGAGC | T | C | Thr | Thr | SILENT- CODING | struct | Human Gene TREMBLNEW- ID:G2961252 SUPERVILLIN - HOMO SAPIENS (HUMAN), 1788 aa. | 0 | 10 |
| 415 | cg43957486 | 1475 | CTGGGGCTCCC CGCTGCCAGTG CCC/A/GJGCCGG CGCCGCCCTGC AGGCAGACG | A | G | Pro | Pro | SILENT- CODING | struct | Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa. | 0.00E+00 | 20 (20p11.2) |
| 416 | cg44932934 | 815 | TGCTCGAGGAT GTCAACCGCAT GTC/G/AJCCCTGG GGCGCTGGCCA TTATCTTCG | G | A | Ser | Ser | SILENT- CODING | struct | Human Gene SPTREMBL-ID:Q63358 MYOSIN HEAVY CHAIN - RATTUS NORVEGICUS (RAT), 1980 aa. | 2.10E-179 | |
| 417 | cg43100187 | 320 | AACGCCCTAGAG GGGAGCTGGT GGC/C/AJCATGA GCCTGCCATCC AGAATGTGC | C | A | Ala | Ala | SILENT- CODING | struct | Human Gene SWISSPROT- ID:P02549 SPECTRIN ALPHA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2418 aa. | 1.80E-169 | |
| 418 | cg42930605 | 333 | GGTCCATGCAC ACCTTGTCCTTC GA/G/AJCCCAGC AGGGCCTTGAG CATGGCAT | G | A | Gly | Gly | SILENT- CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. | 1E-92 | 11 (11p15.5) |
| 419 | cg42930605 | 411 | GGGGCCGCTTG AACTTGCCCCCG CAG/A/GJTCAAA TAGCTTCTGGTT CATGTCCT | A | G | Asp | Asp | SILENT- CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. | 1E-92 | 11 (11p15.5) |

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|-----|------------|-----|---|---|---|-----|-----|-------------------|--------|---|---------|-----------------|
| 427 | cg42930605 | 615 | TCTGCTTCTCTG CCTCAGGCGG CTC/TTCCTCCT TCTCCAGCTCC GTGGCCG | C | T | Glu | Glu | SILENT- CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. | 1E-92 | 11 (11p15.5) |
| 428 | cg42930605 | 621 | TCTCTGCCTCAC GGCGGCTCTCC TC/C/TTCCTCCA GCTCCGTGGCC GCTATCT | C | T | Lys | Lys | SILENT- CODING | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. | 1E-92 | 11 (11p15.5) |
| 429 | cg42893961 | 51 | AATGGCCAGCA GGAAGGCGGG ACC/C/AJGGGC AAGGTGGCAGC CACCAAGCA | C | A | Arg | Arg | SILENT- CODING | struct | Human Gene Similar to SPTREMBL- ID:Q01449 MYOSIN REGULATORY LIGHT CHAIN, CARDIAC MUSCLE ISOFORM - HOMO SAPIENS (HUMAN), 175 aa. | 2.5E-89 | |
| 430 | cg42475816 | 282 | AATCAAGACAAA CCCCAATTGAAA A/G/AJAAAGATTG AAGCCCCACTTTG ATGCCA | G | A | Lys | Lys | SILENT- CODING | struct | Human Gene Similar to SPTREMBL- ID:Q10466 TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 26926 aa. | 7.3E-85 | 2 (2q24.3) |
| 431 | cg42522566 | 337 | TGAAGAACGTAA AGGACCGGGAG GA/T/CJGTGAAG AATGAGGTCAA CATCATGA | T | C | Asp | Asp | SILENT- CODING | struct | Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa. | 6E-55 | |

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|-----|------------|-----|--|---|---|-----|-----|-------------------|----------------------|--|----------|----|
| 432 | cg43297806 | 953 | GTAGATGGGTA GAATAGTAGCC AGG[G/A]ACAAG ACAGCGGTTCT GCAGGGGAGC | G | A | Val | Val | SILENT- CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa | 0.00E+00 | 10 |
| 433 | cg43297806 | 962 | TAGAATAGTAGC CAGGGACAAGA CA[G/A]CGGTTT TGCAGGGAGCG TAGTGCCA | G | A | Arg | Arg | SILENT- CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa | 0.00E+00 | 10 |

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|-----|------------|------|---|---|---|-----|-----|-------------------|----------------------|--|----------|----|
| 436 | cg43297806 | 1016 | GGGCTGGGAG GAGGCTGAAAT CAC[C/T]TGATA GAAGGTATAGTT CAGAGCAA | C | T | Gln | Gln | SILENT- CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcls:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883.aa | 0.00E+00 | 10 |
| 437 | cg43297806 | 1019 | TCTGGGAGGAG GCTGAAATCAC CTG[A/G]TAGAA GGTATAGTTCAG AGCAACTG | A | G | Tyr | Tyr | SILENT- CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcls:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883.aa | 0.00E+00 | 10 |

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|-----|------------|------|---|---|---|-----|-----|-------------------|----------------------|--|----------|----|
| 438 | cg43297806 | 1028 | AGGCTGAAATC ACCTGATAGAA GGT[A/G]TAGTT CAGAGCAACTG GGTCTCCAT | A | G | Tyr | Tyr | SILENT- CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.lpcds:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883.aa | 0.00E+00 | 10 |
| 439 | cg43297806 | 1043 | GATAGAAGGTAT AGTTCAGAGCA ACT[A/GGGTCT CCATGGGCTCG CTGATGCT | T | A | Pro | Pro | SILENT- CODING | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.lpcds:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883.aa | 0.00E+00 | 10 |

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|-----|------------|-----|--|---|---|-----|-----|-------------------|----------|--|----------|--|
| 444 | cg39515668 | 655 | GGCGGAGCCA ACAAGGGCCAG CAG[G]GCCCC AGCAAGACCCT CACCAGAGT | G | C | Ala | Ala | SILENT- CODING | synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.80E-72 | |
| 445 | cg21428405 | 177 | TGACCTCGCCA ATGACAGTGGC AGC[G]AJACACC CCAATGGGCGC AGATCTCCA | G | A | Val | Val | SILENT- CODING | synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.20E-56 | |
| 446 | cg21428405 | 273 | CCTGGGACTCG CTCATGAGGAT CTC[T]C]TCAGG GGCGAGGTTCCG GGTCGCGCA | T | C | Glu | Glu | SILENT- CODING | synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.20E-56 | |
| 447 | cg21428405 | 327 | GAACGCGGTCCG AGCTCGACGTG CAT[G]AJCCACC GTCGCCAGCAC TGGCCAGCT | G | A | Gly | Gly | SILENT- CODING | synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.20E-56 | |
| 448 | cg38924050 | 301 | TCTCGTTGATGA GGTCGTTACCC TC[A]G]CGGGTA CGTTCACCGAC ACCGCGGA | A | G | Arg | Arg | SILENT- CODING | synthase | Human Gene Similar to SWISSPROT- ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa. | 2.60E-53 | |
| 449 | cg38924050 | 310 | TGAGGTCGTTA CCCTCACGGGT ACG[T]C]TCACC GACACCGGCGA AAACCGAAG | T | C | Glu | Glu | SILENT- CODING | synthase | Human Gene Similar to SWISSPROT- ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa. | 2.60E-53 | |

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|-----|------------|------|--|---|---|-----|-----|-------------------|----------|--|-----------|----|
| 450 | cg38924050 | 352 | AAACCGAAGTA CCGCCGAAGTT GTG[G/C]GCGAT ACGGTAAATCAT CTCCTGAA | G | C | Ala | Ala | SILENT- CODING | synthase | Human Gene Similar to SWISSPROT- ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa. | 2.60E-53 | |
| 451 | cg43925970 | 1703 | GAGCACATAAG GTGAAGGTGGT GAC[T/A]CCCAG AGAAAGCGACCT CTATATAGG | T | A | Gly | Gly | SILENT- CODING | tm7 | Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa. | 0.00E+00 | 9 |
| 452 | cg41616031 | 1736 | AAGGGATGTCC CCAAACTTCCAG TC[T/C]GAACGC CGCACATAGTA GTCCATCA | T | C | Ser | Ser | SILENT- CODING | tm7 | Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa. | 2.90E-214 | 12 |
| 453 | cg41616031 | 1744 | TCCCCAAACTTC CAGTCTGAACG CC[G/T]CACATA GTAGTCCATCAC GAACGGC | G | T | Arg | Arg | SILENT- CODING | tm7 | Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa. | 2.90E-214 | 12 |
| 454 | cg41616031 | 1796 | GGCAGATGATC AGTAGAAAGTCA GC[T/C]ACTGCC AGGTTGAACAG GAAAAATCC | T | C | Val | Val | SILENT- CODING | tm7 | Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa. | 2.90E-214 | 12 |

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|-----|------------|-----|---|---|---|-----|-----|-------------------|-----|--|-----------|--|
| 458 | cg42489842 | 432 | TTTGTGAGCAAAG TTGATCAGTCTC TTT/CATACCAA CACATCGCTGG ATGCTG | T | C | Leu | Leu | SILENT- CODING | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa. | 7.30E-106 | |
| 459 | cg42489842 | 456 | TTCATACCAACA CATCGCTGGAT GCTT/CJGCAAGT GAATATGCCAAA TACTGCT | T | C | Ala | Ala | SILENT- CODING | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa. | 7.30E-106 | |
| 460 | cg42489842 | 471 | CGCTGGATGCT GCAAGTGAATAT GC/C/TJAAATACT GCTCAGAAATAT TAGGAG | C | T | Ala | Ala | SILENT- CODING | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa. | 7.30E-106 | |
| 461 | cg42927358 | 947 | TTTTGTCTTTGC CAACATCATCC T[G/A]ACAAATG GTCAGCCAACA GAGGACA | G | A | Leu | Leu | SILENT- CODING | tm7 | Human Gene Similar to SWISSPROT- ID:Q15391 PROBABLE G PROTEIN- COUPLED RECEPTOR KIAA0001 - HOMO SAPIENS (HUMAN), 338 aa. | 1.40E-71 | |

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| 462 | cg42927358 | 544 | ATGAATTGACA CAATTGCTTGC C[G/A]GTGCTTT ATCTCATTATAT TTGTGG | G | A | Pro | Pro | SILENT- CODING | tm7 | Human Gene Similar to SWISSPROT- ID:Q15391 PROBABLE G PROTEIN- COUPLED RECEPTOR KIAA0001 - HOMO SAPIENS (HUMAN), 338 aa. | 1.40E-71 | |
| 463 | cg32423505 | 1056 | CCCTCCTCCTG GCTGAGAAAA GTT[G/T]CCCTT GTGCAAAAAACA CTAGGTACC | G | T | Gly | Gly | SILENT- CODING | tm7 | Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa. | 1.20E-55 | 3 (3q21) |
| 464 | cg43968711 | 2389 | TATGATTGGATG TGGAAGAACTAT C[T/C]GTTGCATT CACATTTAAACG ATTGG | T | C | Thr | Thr | SILENT- CODING | transcript factor | Human Gene SWISSPROT- ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa. | 2.30E-292 | 11 |
| 465 | cg43297259 | 800 | CTCCTGTGTGT GTCCTTAAGTGT CT[G/A]ATGAGG TGTGACTTCTGG CTAAAGC | G | A | Ile | Ile | SILENT- CODING | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa pcds:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 7.80E-54 | |
| 466 | cg20612302 | 301 | TGGAGGCGGCC CACATGGCGGC CAC[C/G]GCCAT CCTCAACCTGTC CACGCGCT | C | G | Thr | Thr | SILENT- CODING | transcript factor | Human Gene Similar to SPTREMBL- ID:O08996 MYELIN TRANSCRIPTION FACTOR 1-LIKE - MUS MUSCULUS (MOUSE), 1182 aa. | 1.70E-53 | |
| 467 | cg43949162 | 856 | GGGCCATGTTA ACCACTTCCTTT TG[C/T]TGATCAT CTGGTTTAAAGA AAGGAT | C | T | Gln | Gln | SILENT- CODING | transferase | Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa. | 1.30E-115 | 6 |

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|-----|------------|------|---|---|---|-----|-----|-------------------|-----------|---|-----------|--|
| 474 | cg44005525 | 1080 | CCTCATACACG GATCTGGAGG CCCT/CJAGAAT GGTTGATCTCCA TTCATAGA | T | C | Leu | Leu | SILENT- CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 | |
| 475 | cg44005525 | 1098 | GAGGCCCTAGA ATGGTTGATCTC CAIT/CJTCATAGA TGTTATCGCCTT TGGGAC | T | C | Glu | Glu | SILENT- CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 | |
| 476 | cg44005525 | 1110 | TGGTTGATCTCC ATTTCATAGATGT TIA/GJTCGCCTTT GGGACCAGCAC TGCAAT | A | G | Asp | Asp | SILENT- CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 | |
| 477 | cg44005525 | 1134 | TATCGCCCTTTGG GACCAGCACTG CAIA/GJTtagGT GGAGGGTCTAA AGTGAITGT | A | G | Asn | Asn | SILENT- CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 | |
| 478 | cg44005525 | 828 | TGTTGGTCATAT ACTGAGTGGCA ATIA/GJCTTCCC ACCAAAGGGTC GGCAGGAT | A | G | Ser | Ser | SILENT- CODING | ubiquitin | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 | |

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|-----|------------|------|--|---|---|-----|-------------------|------------------|--|----------|----------------------|
| 479 | cg17663981 | 225 | CCGAGAACCCG GGCACAGCGAG AGC[C/G]TGGTG CCAAAGTGGCCC AAAAGTTCA | C | G | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa. | 0.00E+00 | 10 (10p11.2 3) |
| 480 | cg17663981 | 234 | CGGGCACAGCG AGAGCCTGGTG CCA[A/G]GTGGC CCAAAAGTTTAC GGCGGGCA | A | G | Gln | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa. | 0.00E+00 | 10 (10p11.2 3) |
| 481 | cg42907760 | 1501 | AACCTGAAGGC CAAAAGTGTGAC TC[G/A]GACTCG GAGAGCACAGT CAGCCCCC | G | A | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa. | 0.00E+00 | 9 (9p12) |
| 482 | cg43301812 | 3795 | CTCCATGGCTG GGATGCTCTGC TGC[G/A]CTTGG TTTTGCCCGAGT GGCAGCCT | G | A | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa. | 0.00E+00 | 3 |
| 483 | cg43917756 | 1098 | AGACACTGACC ACTGGGGGAGG TGC[A/G]GAGAC TGTGCTGGATG TGGTGGAAA | A | G | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q14157 HYPOTHETICAL PROTEIN KIAA0144 - Homo sapiens (Human), 983 aa. | 0.00E+00 | 1 |
| 484 | cg43918356 | 2645 | CATCTTCATCTA GAAACGCCCTC AC[G/T]GAAATG GAATTGCTGCC AGACGTGG | G | T | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment). | 0.00E+00 | 12 |

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|-----|------------|------|--|---|---|-----|-------------------|------------------|---|----------|---|
| 491 | cg43999667 | 3688 | GTACAGCCTGG TAATGGAGAATC AA[A/G]TTTTGCT GTATCGTAAAG GCAGCAA | A | G | Asn | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment). | 0.00E+00 | 6 |
| 492 | cg44009187 | 6789 | TCAACTTGCTCC AGTAGGCCGCC GG[C/T]TCTGCA GGCAGCTCGGG CTGGAAGA | C | T | Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42858 HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN) - Homo sapiens (Human), 3144 aa. | 0.00E+00 | |
| 493 | cg44020180 | 3172 | ATGGGTAGACT CGAGTTTGGTAA AT[G/A]TCCAAA CCATAGGCCAC AACCAAAC | G | A | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 494 | cg44020180 | 3177 | TAGACTCGAGTT TGGTAAATGTCC A[A/G]ACCATAG GCCACAACCAA ACAAAGTG | A | G | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 495 | cg44020180 | 3199 | CCAAACCATAG GCCACAACCAA ACA[A/T]GTGGA CTCCAGACCCG AGGGAGCTG | A | T | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 496 | cg44020180 | 3211 | CCACAACCAA CAAGTGGAATC CAG[A/G]CCCCGA GGGAGCTGTGT AGATACCTC | A | G | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |

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|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|---|----------|---|
| 497 | cg44020180 | 3220 | AACAAAGTGGAC TCCAGACCCGA GGG[A/C]GCTGT GTAGATACCTC GCATTCGAG | A | C | Ala | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 498 | cg44020180 | 3226 | TGGACTCCAGA CCCGAGGGAGC TGT[G/A]TAGATA CCTCGCATTCG AGAAACTG | G | A | Tyr | Tyr | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 499 | cg44020180 | 3232 | CCAGACCCGAG GGAGCTGTGTA GAT[A/G]CCTCG CATTGAGAAAC TGCTGGT | A | G | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 500 | cg44020180 | 3247 | CTGTGTAGATAC CTCGCATTCGA GA[A/G]ACTGTC TGGTTATAGTTG ATGAATC | A | G | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 501 | cg44020180 | 3289 | TGATGAATCGCT CTGCGTGTATCT GT[G]ACATCTG GAGAATACGGG ATTAAGT | T | G | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 502 | cg44020180 | 3298 | GCTCTGCGTGT ATCTGTACATCT GG[A/G]GAATAC GGGATTAAGTTC TCCTCTC | A | G | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |

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|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|---|-----------|---------------------|
| 503 | cg44020180 | 3312 | TGTACATCTGGA GAATACGGGAT TA[A/G]GTTCTC CTCTCTGCTTTG TTCTGTT | A | G | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 504 | cg44020180 | 3319 | CTGGAGAATAC GGGATTAAGTTC TC[C/T]TCTCTGC TTTGTTCTGTTG GGATCT | C | T | Glu | Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment). | 0.00E+00 | 1 |
| 505 | cg44928323 | 2080 | AGCAGGCAGAT AGAAGTTCCTGT CA[C/T]TTTCTCC TTTTTACGGGG TAGGAT | C | T | His | His | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa. | 0.00E+00 | 17 (17q11.2) |
| 506 | cg44932392 | 1281 | TGCTTTGGTTTT TGATAAAATTGT T[G/A]AACTTATT GTTGAGATCAG CGCTGA | G | A | Phe | Phe | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa. | 0.00E+00 | |
| 507 | cg43991434 | 1266 | TCTTGAGCAGA CCCATGTGCAC GAG[G/C]AGCCT GGTGAGGAAGG TGTTGGAGT | G | C | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa. | 1.70E-304 | 22 |
| 508 | cg43985955 | 1994 | GCATGATAGGA TATGGAATTCCT CC[A/T]CAAAATG GGAAGTGTTCC TGTAATGA | A | T | Pro | Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.70E-299 | |
| 509 | cg43985955 | 2009 | GAATTCCTCCAC AAATGGGAAGT GTT[A/C]CTGTAA TGACGCAACCA ACCTTAA | T | A | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.70E-299 | |

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|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|---|-----------|----|
| 510 | cg43985955 | 2021 | AAATGGGAAGT GTTCCCTGTAATG AC[G/A]CAACCA ACCTTAATATAC AGCCAGC | G | A | Thr | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.70E-299 | |
| 511 | cg43985955 | 2060 | TATACAGCCAG CCTGTCATGAG ACC[T/G]CCAAA CCCCCTTGGCC CTGTATCAG | T | G | Pro | Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.70E-299 | |
| 512 | cg44031765 | 2070 | ACCTCGCCGTA GTAGATGTAGC GCA[G/A]CATGG ACTCGAAGGCC TGCCTGCTG | G | A | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa. | 4.60E-279 | 22 |
| 513 | cg43252100 | 466 | TGCAGCCCGA GGTTCCTTTTAC TC[C/A]ATGGTA CCAAATGCAACT ATTACAC | C | A | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA83037 KIAA1085 PROTEIN - HOMO SAPIENS (HUMAN), 584 aa (fragment). | 4.90E-278 | |
| 514 | cg43934178 | 2445 | CGATGCCATGC TTCTCCATGAGC GT[G/A]ATGAGC TCGGCCTCCGT CAGGTAGT | G | A | Ile | Ile | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD29670 DNA TOPOISOMERASE III BETA - HOMO SAPIENS (HUMAN), 862 aa. | 1.80E-274 | |
| 515 | cg43031103 | 1696 | ACATGGCCCTC CCCTTGGTTGA GGA[G/A]ACAGC AGGGGCTGGTG TGAGGTGCA | G | A | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60240 PERILIPIN - HOMO SAPIENS (HUMAN), 522 aa. | 6.30E-266 | |
| 516 | cg43258841 | 340 | TAAATCTTGTGT GGCCATCATCC AG[T/G]GTGTGG AACATTTACCCG TCATCTT | T | G | Thr | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 | |

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|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|---|-----------|--|
| 517 | cg43258841 | 358 | CATCCAGTGTGT GGAACATTTTCAC C[G/A]TCATCTTC TACTGGTATAAT TTGAA | G | A | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 | |
| 518 | cg43258841 | 370 | GGAACATTTTCAC CGTCATCTTCTA C[T/G]GGTATAA TTTGAAAGTGCT TTATTT | T | G | Pro | Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 | |
| 519 | cg43258841 | 388 | CTTCTACTGGTA TAATTTGAAAGT G[C/T]TTTATTT TTGTCCATGACT CATTG | C | T | Lys | Lys | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 | |
| 520 | cg43258841 | 394 | CTGGTATAATTT GAAAGTGCTTTA T[T/C]TTTTGTCC ATGACTCATTGA CAGTA | T | C | Lys | Lys | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 | |
| 521 | cg43258841 | 403 | TTTGAAAGTGCT TTATTTTGTGTC C[A/G]TGACTCA TTGACAGTACGA AAGTTT | A | G | His | His | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 | |
| 522 | cg43258841 | 421 | TTTGTCCATGAC TCATTGACAGTA C[G/A]AAAGTTT GGGGTACTCT GACTAT | G | A | Phe | Phe | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 | |
| 523 | cg43258841 | 484 | AAACTCCATCCA CAAGTCCTTGCT G[A/G]ATAATCA ATCGCTGAGCC TCATCTC | A | G | Ile | Ile | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 | |
| 524 | cg43258841 | 493 | CCACAAGTCCTT GCTGAATAATCA A[T/C]CGCTGAG CCTCATCTCTAG AAATTT | T | C | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 | |

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|-----|------------|------|---|---|---|-----|-----|-------------------|------------------|--|-----------|-----------------|
| 532 | cg42676981 | 1712 | GGAAGTAGAGG TCAGGTGGGC TGT[G]AGGCT CTTCAGGTTCAA ACACCGGA | G | A | Pro | Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa. | 5.90E-231 | 15 |
| 533 | cg43918561 | 843 | GGAAGGAGGTC TACACCACGCT GAA[G]AGGCT CTACGCCACGC ACGCCTGCG | G | A | Lys | Lys | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P04177 TYROSINE 3- MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3-HYDROXYLASE) (TH) Rattus norvegicus (Rat), 498 aa. | 2.10E-224 | 11 (11p15.5) |
| 534 | cg43999712 | 566 | ACGTACCAAATG AAATGCTCTACG G[G]CJCGAATAG GCTACATCTATG CTCTGC | G | C | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa. | 3.30E-221 | 2 |
| 535 | cg43999712 | 569 | TACCAAATGAAA TGCTCTACGGG CG[A]CJATAGGC TACATCTATGCT CTGCTTT | A | C | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa. | 3.30E-221 | 2 |
| 536 | cg43999712 | 659 | GCCATATTCAGC AGATTTGTGAAA C[A]CJATTTTAAC CTCTGGAGAAA ACCTAT | A | C | Thr | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa. | 3.30E-221 | 2 |
| 537 | cg43922139 | 1860 | ACTTGACTTTCC AGACACGGTGA GG[A]GJAGGAGG AGGCTGTCGGG ACCAAACG | A | G | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O88473 RJS - MUS MUSCULUS (MOUSE), 4836 aa. | 2.80E-218 | |
| 538 | cg43955639 | 512 | CAGGCATGGTG ATGAGGGGTGC TGG[G/T]GCCAG GGAGGTGGCAG GAGCTGGCA | G | T | Ala | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment). | 2.80E-215 | |

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|-----|------------|------|---|---|---|-----|-----|-------------------|------------------|--|------------------------|----|
| 546 | cg43918701 | 1667 | TTTTCCAGATGC GACAGACATCAT TTT/CJGGGCATA TTCTAGAAACCA AGGGCA | T | C | Pro | Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60736 KE03 PROTEIN - HOMO SAPIENS (HUMAN), 367 aa (fragment). | 1.10E-170 | |
| 547 | cg43926685 | 815 | AGAATTCCTTAC TGGATCACCGC AA[C/T]AAGACC ATCCACAACGAT TACCGCA | C | T | Asn | Asn | SILENT- CODING | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa. | 2.50E-168 (1p36.33) | |
| 548 | cg44927654 | 263 | GTGCCAGCTTC TCCATGGTGGC ATC[C/T]GTCAG GATGCTGGGT AGGGAGGTT | C | T | Thr | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA74865 KIAA0842 PROTEIN - HOMO SAPIENS (HUMAN), 1020 aa (fragment). | 7.3E-165 | |
| 549 | cg43993462 | 2019 | CCAACTCATTGA CAGTGAGGGGT GC[G/A]TCTCCA CTTCTGTTGGTG TAATTGA | G | A | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment). | 5.1E-161 | 5 |
| 550 | cg44010310 | 1180 | CTATATTCTCTG ATTGTGCAAAAGT A[C/T]AGGACAT TATATTCGACAT CTTTGG | C | T | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA32101 BCAP - HOMO SAPIENS (HUMAN), 331 aa. | 1.3E-155 | 13 |
| 551 | cg43950590 | 1319 | GGTGCAACCATG TACAGCTGCCC AAT[C/T]TGAGA GAAGAATCCTC CGACGGGCTT | C | T | Gln | Gln | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.9E-154 | 7 |
| 552 | cg43950590 | 1334 | GCTGCCCAATC TGAGAGAAGAA TCC[T/C]CCGAC GGCTTCGTTAC CATCCTGTC | T | C | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |

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|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|---|-----------|----|
| 553 | cg43950590 | 1361 | CGACGGCTTCG TTACCATCCTGT CT[G/A]AAGCGG ATTGCACGAGC CCAGTAAT | G | A | Phe | Phe | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 554 | cg43950590 | 1370 | CGTTACCATCCT GTCTGAAGCGG ATT[G/G]GCACGA GCCAGTAATT GCCCCATT | T | G | Ala | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 555 | cg43950590 | 1376 | CATCCTGTCTGA AGCGGATTGCA CG[A/G]GCCCCAG TAATTGCCCCAT TCAATCA | A | G | Ala | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 556 | cg43950590 | 1397 | CACGAGCCCCAG TAATTGCCCCAT TC[A/G]ATCATG GTTCTTGGTCG GAGTTGGT | A | G | Ile | Ile | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 557 | cg43950590 | 1436 | GTCGGAGTTGG TAAGACCTGAGT TC[A/G]TATATAT TAGGTCCGGAT CTTGGCA | A | G | Tyr | Tyr | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 558 | cg43950590 | 1445 | GGTAAGACCTG AGTTCATATATA TT[A/G]GGTCCG GATCTTGGCAC AGGCTCAT | A | G | Pro | Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 559 | cg43951092 | 1484 | GAGTAGAATTCA AGAAGAGTTCAA TTA/GTATCGAT GTTGCATGTTAT TTTTAT | A | G | Tyr | Tyr | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |

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|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|---|-----------|----|
| 560 | cg43951092 | 1526 | TATTTTATCTTT AGACATGGCAG CTT/CJACTGCAT CTTCATGTGTCA CAAACT | T | C | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |
| 561 | cg43951092 | 1583 | CTGCTTCTCCTG TGCTCTGCTGCA TC[A/G]GCTCCA ATATCAATATGA ACTCGTA | A | G | Ala | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |
| 562 | cg43951092 | 1604 | CATCAGCTCCAA TATCAATATGAA CTT/GJCGTATTG GATTAGTGGTG AGAAGA | T | G | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |
| 563 | cg43951092 | 1616 | TATCAATATGAA CTCGTATTGGAT TTT/GJAGTGGTG AGAAGAAATTAG CAATGT | T | G | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |
| 564 | cg43951092 | 1640 | TTAGTGGTGAG AAGAAATTAGCA AT[G/A]TCATTTT CAGTTGCACGA AAAGGCA | G | A | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |
| 565 | cg43990820 | 1135 | CATCAGTTTCCA CTTCGACACATC G[G/A]TAGTCCT CACAGCCACGG CCATCCA | G | A | Tyr | Tyr | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 3.30E-150 | 3 |
| 566 | cg43990820 | 724 | TCGACCCCTCTT CATCCTCCAAAA CTT/CJCGAACCC TTGGTATCCTTG TATTGA | T | C | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment). | 3.30E-150 | 3 |

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|-----|------------|-----|--|---|-----|-------------------|------------------|---|-----------|--|
| 572 | cg29351416 | 546 | AGTTCCAAAGTAG ACAACAGTAATC G[C/T]CTGTTACT GCAGCAGGTCT CATTAC | T | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. | 3.20E-127 | |
| 573 | cg29351416 | 645 | TGTATGCTCAGA CCACGCTGAGA TA[C/T]AACATGC CCTTGGAGAAG CAGCAGC | T | Tyr | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. | 3.20E-127 | |
| 574 | cg29351416 | 648 | ATGCTCAGACC ACGCTGAGATA CAA[C/T]ATGCC CTTGGAGAAGC AGCAGCCTG | T | Asn | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. | 3.20E-127 | |
| 575 | cg43950273 | 530 | GGTCTTCAATAA AGTAGTTATGGC A[C/A]GTCCTGA TCCACATAGATA GCTGAA | A | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB45700 HYPOTHETICAL 32.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 287 aa (fragment). | 2.40E-123 | |

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|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|--|-----------|--|
| 580 | cg44930828 | 603 | CTCGAGGTGAG AAACCCCAATCCT TT[G/A]AGGCAA AAGAACGCCAA GGTGAACC | G | A | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLDHIDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLDHIDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 | |
| 581 | cg44930828 | 615 | AACCCCAATCCTT TGAGGCAAAAG AA[C/T]GCCAAG GTGAACCAACT CCTCAAGG | C | T | Asn | Asn | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLDHIDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLDHIDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 | |
| 582 | cg44930828 | 630 | GGCAAAAAGAAC GCCAAGGTGAA CCA[A/G]CTCCT CAAGGTTTCGCT GCCGAAAGC | A | G | Gln | Gln | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLDHIDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLDHIDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 | |
| 583 | cg44930828 | 645 | AGGTGAACCAA CTCCTCAAGGTT TC[G/C]CTGCCG AAGCTTGCCAA CGTGCAGC | G | C | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLDHIDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLDHIDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 | |

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|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|--|-----------|--|
| 584 | cg44930828 | 663 | AGGTTTCGCTG CCGAAGCTTGC CAA[C/T]GTGCA GCTCCTGGATA CCGACGGGG | C | T | Asn | Asn | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 | |
| 585 | cg44930828 | 690 | TGCAGCTCCTG GATACCGACGG GGG[T/C]TTGT GCACTCGGACG GTGCCATCT | T | C | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 | |
| 586 | cg44930828 | 693 | AGCTCCTGGAT ACCGACGGGG TTT[T/C]GTGCAC TCGGACGGTGC CATCTCCT | T | C | Phe | Phe | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 | |
| 587 | cg43975478 | 691 | AAACCCCTGAG AAAAGATACAAT GT[C/T]CTGGGA GCTGAGACTGT GCTCAATC | C | T | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q63555 SP120 - RATTUS NORVEGICUS (RAT), 798 aa. | 4.10E-119 | |
| 588 | cg42530218 | 601 | GCATGCCCCAGT AATAAAGATGAA GAT[C/G]GGGCTA GTGGTTTGTAGTT TTCAACA | T | C | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa. | 2.00E-118 | |

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|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|--|-----------|----|
| 596 | cg43986282 | 794 | GCACCTCTTCTG CGTGGTACACG GT[C/T]CTCCCA CAGGCCCCACA CTTGTTTC | C | T | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 597 | cg43986282 | 800 | CTTCTGCGTGG TACACGGTCCT CCC[A/G]CAGGC CCCACACTTGT TCCACCTC | A | G | Cys | Cys | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 598 | cg43986282 | 809 | GGTACACGGTC CTCCACAGGC CCC[A/G]CACTT GTTCCACCTCC CCAGACAG | A | G | Cys | Cys | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 599 | cg43986282 | 815 | CGGTCCTCCCA CAGGCCCCACA CTT[G/A]TTTCCA CCTCCCCAGAC AGGCATTTC | G | A | Asn | Asn | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa. | 2.90E-110 | 12 |
| 600 | cg42723058 | 651 | GTCCCTTACCA CCACCGGTCAC AGA[T/C]GTGAG CCTTGAGTTGCA GCAGCTGC | T | C | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA82158 HCR PROTEIN - HOMO SAPIENS (HUMAN), 756 aa. | 1.70E-107 | |
| 601 | cg42723058 | 673 | AGATGTGAGCC TTGAGTTGCAG CAG[C/T]TGCGG GAAGAACGGAA CCGCCTGGA | C | T | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA82158 HCR PROTEIN - HOMO SAPIENS (HUMAN), 756 aa. | 1.70E-107 | |

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|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|---|-----------|----|
| 609 | cg44911139 | 722 | GCAAGGTTTCG GATGTACGTATC ATC/TTCAGATC GGAACACACGT CGTCTA | C | T | Ile | Ile | SILENT- CODING | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q1499 SPLICING FACTOR - HOMO SAPIENS (HUMAN), 530 aa. | 7.90E-101 | 14 |
| 610 | cg42539705 | 165 | AAAGGAACTAT TTCCAGATGAG GC[G/A]GGGTGT CTGGAGGGGC TGTGGGTG | G | A | Pro | Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75229 R31449_3 - HOMO SAPIENS (HUMAN), 813 aa (fragment). | 1.20E-100 | |
| 611 | cg42028329 | 115 | CCAAGGAGAAC CCGTGCAGAA ATT[C/T]CAGGC CAACATCTTCAA CAAGAGCA | C | T | Phe | Phe | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |
| 612 | cg42028329 | 277 | ACTTTGACAACC CAGTACACCGG TC[T/A]CGGAA TGGCAGCGACG GTTCTTCA | T | A | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |
| 613 | cg42028329 | 295 | ACCGGTCTCGG AAATGGCAGCG ACG[G/A]TTCTT CATCCTTTACGA GCACGGCC | G | A | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |
| 614 | cg42028329 | 310 | GGCAGCGACGG TTCCTCATCCTT TA[C/T]GAGCAC GGCCTCTTGGC CTACGCC | C | T | Tyr | Tyr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |
| 615 | cg42028329 | 316 | GACGGTCTTCA TCCTTTACGAGC A[C/T]GGCCTCT TGCCTACGCC CTGGATG | C | T | His | His | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |

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|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|--|----------|--|
| 616 | cg42028329 | 328 | TCCTTTACGAGC ACGGCCTCTTG CGC/AJTACGCC CTGGATGAGAT GCCACAGA | C | A | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |
| 617 | cg42028329 | 352 | GCTACGCCCTG GATGAGATGCC CAC/GCJACCCT TCCTCAGGGCA CCATCAACA | G | C | Thr | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa. | 2.40E-99 | |
| 618 | cg42392719 | 540 | TCGCGAGAACG GCCTCAGTGCC AAG[G/T]CCCTT ACCCCTGCAGC TGGGCTCTG | G | T | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa. | 6.40E-99 | |
| 619 | cg42392719 | 606 | TCTCCCCCAAG GTGGGGTCTTC TAG[A/G]TCTGT GAGGAAGAGGT TCACATCTC | A | G | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa. | 6.40E-99 | |
| 620 | cg42392719 | 627 | CTAGATCTGTGA GGAAGAGGTTT AC[A/G]TCTCCC ACCATGCAGCT CTCTTCAG | A | G | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa. | 6.40E-99 | |
| 621 | cg39512856 | 597 | ACGCGTCGCCG GAAGCCACGTC ATA[G/A]ACGGT TTTACCCCGATG GTCTTCAA | G | A | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 622 | cg39512856 | 615 | CGTCATAGACG GTTTACCCCGA TG[G/A]TCTTCAA CGAGATGCCAC GATGCCT | G | A | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |

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|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|---|----------|----|
| 623 | cg39512856 | 663 | CCTCATCACTGT TGAAACAGCC AC/A/GAAGCCA GCCGGAATATC TGGCGGTG | A | G | Phe | Phe | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 624 | cg39512856 | 690 | AGCCAGCCGGA ATATCTGGCGG TGC/A/GATATC GGTACTGTTTGC AGCAGAC | A | G | Ile | Ile | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 625 | cg39512856 | 708 | GCGGTGCAATA TCGGTACTGTTT GC/A/TGGCAGA CCGGTATGAGG CGGAATAT | A | T | Pro | Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 626 | cg39512856 | 717 | TATCGGTACTGT TTGCAGGCAGA CC/G/TGTATGA GGCGGAATATA TGCGTAC | G | T | Thr | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 627 | cg37445474 | 599 | CCCTGCAAGCT CTGTATGGAAC GATC/TCCCCA GATCTTTGGGA AGGAGAAT | C | T | Ile | Ile | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q63615 VACUOLAR PROTEIN SORTING HOMOLOG R-VPS33A - RATTUS NORVEGICUS (RAT), 597 aa. | 2.80E-96 | |
| 628 | cg30791729 | 294 | CAGATCCAGTG GCCTTCCCCCA GCTG/TJGTCA ACTGTGTCCAG GCTGTGGCT | G | T | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P12346 SEROTRANSFERRIN PRECURSOR (SIDEROPHILIN) (BETA-1-METAL BINDING GLOBULIN) - Rattus norvegicus (Rat), 698 aa. | 3.20E-95 | |
| 629 | cg42522690 | 454 | GTGAACAGTGT AAATCAGTTTT CA/T/CJTGGGAC ATGAAATCCAAG GATAAGG | T | C | His | His | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35884 NEBULIN-RELATED ANCHORING PROTEIN (N-RAP) - MUS MUSCULUS (MOUSE), 1175 aa. | 3.30E-94 | 10 |

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|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|---|----------|----|
| 630 | cg42522690 | 625 | CTCGAAAGTCTC TTGGTGAGGAA TA[T/C]ACAGAA GACTATGAGCA ACCCAGGG | T | C | Tyr | Tyr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O35884 NEBULIN-RELATED ANCHORING PROTEIN (N-RAP) - MUS MUSCULUS (MOUSE), 1175 aa. | 3.30E-94 | 10 |
| 631 | cg43982164 | 561 | AGGTCTACGTG TTGAAGCGTCCT CA[T/C]GTGGAT GAGTTCCTGCA GCGAATGG | T | C | His | His | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15194 HYA22 - HOMO SAPIENS (HUMAN), 340 aa. | 1.00E-90 | |
| 632 | cg43980889 | 755 | AAGACCAATTAC AAGTAGAAAATG AT[C/G]CTTACC CTGGTACCGAT AGAACAG | T | C | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 633 | cg43980889 | 770 | TAGAAAATGATG CTTACCCTGGTA C[C/T]GATAGAA CAGAAAATGTTA AATATA | C | T | Thr | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 634 | cg43980889 | 776 | ATGATGCTTACC CTGGTACCGAT AG[A/G]ACAGAA AATGTTAAATAT AGACAAG | A | G | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 635 | cg43980889 | 791 | GTACCGATAGA ACAGAAAATGTT AA[A/G]TATAGA CAAGTGGACCA TTTTGCCT | A | G | Lys | Lys | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |
| 636 | cg43955651 | 449 | CTTCCACCCACG CCTGTGTTCTG GGC[G/A]CTGAC AAAGGCCACCT TGTTGGTGT | G | A | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD27745 CGI- 36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa. | 1.10E-87 | 2 |

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|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|--|----------|---|
| 637 | cg43956651 | 476 | TGACAAAGGCC ACCTGTGGTG TC[G/A]GGCTTG AGCGGAATGAA GCCACACT | G | A | Pro | Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD2745 CGI- 36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa. | 1.10E-87 | 2 |
| 638 | cg42353267 | 1516 | GGCCTTCGATC CAGTCCATGAG CAA[T/C]GCCAT ATAGCGCGGCG CAGAGAGCT | T | C | Ala | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75249 R26660_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 291 aa (fragment). | 2.60E-86 | |
| 639 | cg37027086 | 258 | GGGTTCTTCAAC TGGGACAGGAG GC[T/C]TCTACC CACCAGGCCCA AAACGAGG | T | C | Ala | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA76824 KIAA0980 PROTEIN - HOMO SAPIENS (HUMAN), 1406 aa (fragment). | 1.20E-83 | |
| 640 | cg42688841 | 449 | TCAACATAAGGT AGAAATTCATTA A[C/T]CTCAAGA AGCGAGCGTCA TAGTATA | C | T | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 | |
| 641 | cg42688841 | 454 | ATAAGGTAGAAT TTCATTAACCTC A[A/G]GAAGCGA GCGTCATAGTAT AAAAGAA | A | G | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 | |
| 642 | cg42688841 | 461 | AGAAATTCATTA ACCTCAAGAAAG CG[A/G]GCGTCA TAGTATAAGAA GGCTTGA | A | G | Ala | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 | |

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|-----|------------|------|--|---|---|-----|-------------------|------------------|--|----------|---|
| 643 | cg4268841 | 476 | TCAAGAAGCGA GCGTCATAGTAT AA[A/G]GAAGGC TTGACGACAAAC AGTCTCT | A | G | Ser | Silent- Coding | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 | |
| 644 | cg43982291 | 1590 | CACTGTGACCAT TTTGTACAGCAA G[A/C]JAGCAGCG GTATATTCCCAT CCAAAT | A | C | Leu | Silent- Coding | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q28282 C3VS PROTEIN - CANIS FAMILIARIS (DOG), 659 aa. | 3.20E-79 | |
| 645 | cg43982291 | 1716 | GTAAAGCTGTTT TCCCAGAGCTG TC[G/A]JACACTTT CGGCTGGGCAT TTAGACT | G | A | Val | Silent- Coding | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q28282 C3VS PROTEIN - CANIS FAMILIARIS (DOG), 659 aa. | 3.20E-79 | |
| 646 | cg44003673 | 320 | CATGCTTGGTG CCTGGTGCCAG GTG[A/G]GTGAT GACGACCTCCA CGGCCTGCA | A | G | Thr | Silent- Coding | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa. | 1.60E-77 | |
| 647 | cg44003673 | 449 | CATCAGAGATGT GCAGGAAGATG TC[G/A]GGGCCG CCATCAGCTGG GGTAATGA | G | A | Pro | Silent- Coding | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa. | 1.60E-77 | |
| 648 | cg44003673 | 470 | TGTCGGGGCCG CCATCAGCTGG GGT[A/G]ATGAA GCCATGGCCCT TGGACCGGC | A | G | Ile | Silent- Coding | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa. | 1.60E-77 | |
| 649 | cg44936941 | 1207 | CGCGCACCTCG TCGCCGATCTG CTGT[C]CCCGT CTCCTTGCCGA GGAAGTCGT | T | C | Gly | Silent- Coding | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa. | 7.00E-77 | 1 |

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|-----|------------|-----|--|---|---|-----|-------------------|------------------|--|----------|--|
| 650 | cg39523553 | 704 | GGTCTGCCCGA TCCGGGATGGC TGC[A]GGTGG GTGATCGACGG TAGGCCGGA | C | A | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 | |
| 651 | cg39523553 | 721 | ATGGCTGCCCG TGGGTGATCGA CGG[T/C]AGGCC GGACAATGCC CGGCCCGTC | T | C | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.2E-75 | |
| 652 | cg39523553 | 772 | GAGGACAGCCA TGGAAAGGGCAC GGA[T/C]CGCCA GTGCCCGCGCG TGATTATGG | T | C | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.2E-75 | |
| 653 | cg39523553 | 823 | ACGTGGTGCGC AACAGCCCTCA CGG[A/G]GTGAA GGTCCAGATGG CTCTTTCCG | A | G | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.2E-75 | |
| 654 | cg39523553 | 874 | CCTGGCCCGAG CTCGATCAGGC ATC[A/G]AGGTG CCTGGAATCCTT ACTCGATG | A | G | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.2E-75 | |
| 655 | cg39523553 | 886 | TCGATCAGGCA TCAAGGTGCCT GGA[A/G]TCCTT ACTCGATGACG GTTTAGTGC | A | G | Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.2E-75 | |

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|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|--|----------|----|
| 656 | cg36728314 | 399 | GCTGCTGCTTCT TCCTTGTTGGAA C[G/A]ATCTTCT GGGCAACGTCC TGGAAGA | G | A | Ile | Ile | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa. | 1.3E-73 | |
| 657 | cg41677120 | 375 | TTCAGTGCACAA ATGAGATGAATG T[G/T]AACATCC CACAGTTGGCA GACAGTT | G | T | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 1.10E-71 | 11 |
| 658 | cg44126579 | 655 | AGGAGTATTCAT CATCCCCAATG CC[G/A]TAGCCT TCATGATTGAGG AATTGTC | G | A | Tyr | Tyr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa. | 1.10E-71 | 16 |
| 659 | cg44126579 | 712 | GAGTGGCCCAG CCAAATCTGCATG AC[G/A]CCAGAA GTGACCACTGTT ACTTCAT | G | A | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa. | 1.10E-71 | 16 |
| 660 | cg38925480 | 73 | AGAAATCTCACCA GCCTTGTGGTG CT[G/A]CATTG CATAACAACCG CATCCAGC | G | A | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O75473 ORPHAN G PROTEIN- COUPLED RECEPTOR HG38 - HOMO SAPIENS (HUMAN), 907 aa. | 4.90E-69 | |
| 661 | cg43323149 | 544 | GCACACGCGGA AGCCCTACAGA CG[G/A]CTCAG CGTCATGCAAG GGCCCTACA | A | G | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa. | 1.00E-68 | 1 |
| 662 | cg43323149 | 559 | CTACAGACGGA CTCAGCGTCAT GCAI[A/G]GGGCC CTACAGCGAAA CAGCCAGCT | A | G | Gln | Gln | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa. | 1.00E-68 | 1 |

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|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|--|----------|---|
| 663 | cg43323149 | 664 | GAAATACAGC CGGTTAGAGTT CA[A/G]GCCGAT GTCCAAAAGGA AATTTTCC | A | G | Gln | Gln | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa. | 1.00E-68 | 1 |
| 664 | cg34243633 | 263 | CCACCACAGAG ATAATGCAGGC CAG[G/C]GAGGA GATTGCACTGG ATGTCACCA | G | C | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. | 1.3E-68 | |
| 665 | cg34243633 | 431 | CAACTGCTGTCA CAATGCTGGCA CC[G/A]ACATAA GAAC TTGTTTC CAGCTGG | G | A | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. | 1.3E-68 | |
| 666 | cg34243633 | 482 | GGAGCAGCATG GCAACCAGTGT GCC[C/T]AAAAG CCCCAGAAGGC CTAGGATGT | C | T | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. | 1.3E-68 | |
| 667 | cg43942922 | 231 | AGCCCACATCT CAGGCCACTAG GGG[C/A]AGAAC AAATAGGTCCTC TGTC AAGA | C | A | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.3E-68 | |
| 668 | cg43942922 | 291 | CAGTTGTCCCC ACAGCCCCTGA GCT[C/T]CAGCC TTCCACCTCCAC AGACCAGC | C | T | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.3E-68 | |

| Variable | Mean | SD | Min | Max |
|---------------------------|------|------|-----|------|
| Age | 34.5 | 10.2 | 21 | 55 |
| Gender | 0.5 | 0.5 | 0 | 1 |
| Marital status | 0.6 | 0.5 | 0 | 1 |
| Education | 12.5 | 1.5 | 9 | 16 |
| Income | 1500 | 500 | 500 | 3000 |
| Health status | 0.8 | 0.2 | 0 | 1 |
| Employment status | 0.7 | 0.4 | 0 | 1 |
| Family size | 3.2 | 1.1 | 1 | 6 |
| Home ownership | 0.9 | 0.1 | 0 | 1 |
| Vehicle ownership | 0.6 | 0.5 | 0 | 1 |
| Travel frequency | 2.5 | 1.5 | 0 | 6 |
| Travel distance | 150 | 50 | 50 | 300 |
| Travel mode | 0.4 | 0.4 | 0 | 1 |
| Travel cost | 100 | 30 | 50 | 200 |
| Travel satisfaction | 0.7 | 0.3 | 0 | 1 |
| Travel frequency (log) | 0.4 | 0.2 | 0 | 1 |
| Travel distance (log) | 0.2 | 0.1 | 0 | 1 |
| Travel cost (log) | 0.1 | 0.1 | 0 | 1 |
| Travel mode (log) | 0.0 | 0.0 | 0 | 1 |
| Travel satisfaction (log) | 0.0 | 0.0 | 0 | 1 |

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|-----|------------|------|---|---|---|-----|-----|-------------------|------------------|--|---------|--|
| 669 | cg43942922 | 396 | CTGTCAAGACC CCTGAACAGTT GT[G/C]CCACACA GCCCTGAGCT CCAGCCTT | G | C | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.3E-68 | |
| 670 | cg43955219 | 1090 | CCTGGCCAACA TGGCAAAACCC CGT[C/T]TCTACT AAAAATACAAA AGCCGGG | C | T | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P39194 !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa. | 6.4E-68 | |
| 671 | cg29142822 | 401 | CACCTCACA AAAA GGCAAGAAAGC GC[A/G]AGGAGG GATAATGCTTG GAAGCCA | A | G | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q07320 ZEIN-ALPHA PRECURSOR (ZSF4C4) - ZEA MAYS (MAIZE), 266 aa. | 2.5E-65 | |
| 672 | cg43988710 | 397 | TTGGTGAAGAG GTTGTACAGCA CTC[G/T]TAGTG TAGACTTCAGGT CACAGTTG | G | T | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD34051 CGI- 56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa. | 1.4E-62 | |
| 673 | cg43988710 | 404 | AGAGGTTGTAC AGCACTCGTAG TG[A/G]GACTT CAGGTCACAGT TGACAAATGT | A | G | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD34051 CGI- 56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa. | 1.4E-62 | |
| 674 | cg39516123 | 1049 | GCTTGGACCCGG CATGTGGCCTAT GGT[C/G]GGCTAT TCTACCCCGGA GGATCGGA | T | C | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 5.1E-62 | |
| 675 | cg39516123 | 452 | CAGGCAGCCTG GGACAGCCCGAG CCC[G/A]TCTGC CCAGAGAAACT ACCAGAGCT | G | A | Pro | Pro | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 5.1E-62 | |

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|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|---|----------|--|
| 676 | cg39516123 | 563 | TCAGCTCCTCTC CGGAAAGCCAG GC[C]CGAGCT CAGTTCAGTGT GGCTGGCG | C | T | Ala | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 5.1E-62 | |
| 677 | cg39516123 | 620 | CGGTGCCTGGG AGCCCTCAGGC GCG[C]T]CACAG AACAGTGGGCA CCAACAGTC | C | T | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 5.1E-62 | |
| 678 | cg42731307 | 435 | GGAATGAGCC AAAGTTCGCATG AA[T]C]CCACGG AAGTTTACCTGG TCCTCTC | T | C | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.6E-61 | |
| 679 | cg44128084 | 440 | CCGGACAACAC CGTTGGAGTTCT TT[T]C]GCCGTC AACGAGTTGTCT CTGGAAA | T | C | Phe | Phe | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.70E-59 | |
| 680 | cg44128084 | 665 | TGAGCGCTCAC GCTCTCTTTGCT CG[A]G]CCGCTG GTCATGAGCCC AGCTGCTC | A | G | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.70E-59 | |
| 681 | cg44128084 | 680 | TCTTTGCTCGAC CGCTGGTCATG AG[C]T]CCAGCT GCTCGAGTGGA CCTTGACA | C | T | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.70E-59 | |
| 682 | cg44128084 | 695 | TGGTCATGAGC CCAGCTGCTCG AGT[G/A]GACCT TGACATCCAGC CAGACGGTT | G | A | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.70E-59 | |

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|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|---|----------|--|
| 690 | cg43153425 | 128 | GTGACCGAGAG ATCAGCATGTCT GTCTGGTCTG GGAAGGTCACA GTTAGACT | C | T | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 | |
| 691 | cg43153425 | 140 | TCAGCATGTCTG TCGGTCTGGGA AG[G/A]TCACAG TTAGACTCCAAA GGAGGAG | G | A | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 | |
| 692 | cg43153425 | 146 | TGTCTGTCTGGT CTGGGAAGGTC ACA[G/A]TTAGA CTCCAAAGGAG GAGTAGTTG | G | A | Gln | Gln | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 | |
| 693 | cg43153425 | 152 | TCGGTCTGGGA AGGTCACAGTTA GA[C/T]TCCAAA GGAGGAGTAGT TGGTGGGA | C | T | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 | |
| 694 | cg43153425 | 155 | GTCTGGGAAGG TCACAGTTAGAC TC[C/T]AAAGGA GGAGTAGTTGG TGGGACCA | C | T | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 | |
| 695 | cg43153425 | 251 | CAAATCAGCAAC CAAACCAACAAA T[A/T]CAAAATTAC TATGGGTTCTAC TGAAT | A | T | Ile | Ile | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 | |
| 696 | cg43153425 | 287 | TGGGTTCTACTG AATCTCGGGTT GA[C/T]TACATG GGCTCAAGCAT CCTCATGG | C | T | Asp | Asp | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 | |

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|-----|------------|------|---|---|---|-----|-----|-------------------|------------------|--|----------|--|
| 697 | cg30384142 | 40 | CTTGCGCGGCA CCAGGCGGTAA GAC[G/A]ACCCA TATTTAGAACT GGCACCTC | G | A | Thr | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P44788 SUN PROTEIN (FMU PROTEIN) - Haemophilus influenzae, 451 aa. | 5.30E-56 | |
| 698 | cg44015614 | 1289 | GCTCTGGCTGG GGTGCACTATA CTT[C/T]TCCAC GTATTCTATTTC CACAACTT | C | T | Glu | Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 | |
| 699 | cg44015614 | 1295 | GCTGGGTGCA GTACTTCTCC AC[G/A]TATTCTA TTTCCACAACCT CTTCTG | G | A | Tyr | Tyr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 | |
| 700 | cg44015614 | 1313 | TCTCCACGTATT CTATTTCCACAA C[T/C]TCTTCTGA TGAGATGTTCTC CATT | T | C | Glu | Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 | |
| 701 | cg44015614 | 1319 | CGTATTCTATT CCACAACCTCT C[T/C]GATGAGA TGTTCTCCATTT CCATGT | T | C | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 | |
| 702 | cg44015614 | 1325 | CTATTTCCACAA CTTCTTCTGATG A[G/A]ATGTTCTC CATTTCATGTC TTTGT | G | A | Ile | Ile | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 | |

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|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|--|----------|----|
| 703 | cg44015614 | 1379 | AGGGCATTGCG AGAAACTGGCC CTT[A/G]ATAAG GAAATCAAACCTC CACATGTT | A | G | Ile | Ile | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 | |
| 704 | cg42380652 | 406 | AGTCCAGGCG GGGCCACGTC CTC[T/C]CGTA CACCTTTCCAG GAAGGGC | T | C | Arg | Arg | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62739 RABIN3 - RATTUS NORVEGICUS (RAT), 460 aa. | 4.20E-54 | |
| 705 | cg43931038 | 425 | TCTTCTCTAGAG TCCCGCGGCTC AC[A/G]GCCTTT GCTGCGAAGGG CAACTTGT | A | G | Ala | Ala | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 706 | cg43931038 | 436 | GTCCCGCGGCT CACAGCCTTTG CTG[C/G]GAAGG GCAACTTGTGG GCAACCTGG | C | G | Ser | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 707 | cg43931038 | 463 | AAGGGCAACTT GTGGGCAACCT GGT[C/T]AAGGA AACCTTGACTTC TTCAAATT | C | T | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 708 | cg43931038 | 469 | AACTTGTGGGC AACCTGGTCAA GGA[A/C]ACCTT GACTTCTTCAA TTCACAAC | A | C | Val | Val | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 709 | cg43931038 | 478 | GCAACCTGGTC AAGGAAACCTT GACT[C/T]CTTCA AATTCACAACGC CCACCCA | T | C | Glu | Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |

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|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|---|----------|----|
| 710 | cg43931038 | 496 | CCTTGACTTCTT CAAATTCACAAC GIC/TJCCACCA TCTCTACAACAA GGCGGC | C | T | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 711 | cg43931038 | 562 | TCACGTAAGTGG TCAATAGCACCT TTIGAJCCTCCC CCCATGCGATG CCCAACAC | G | A | Gly | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 712 | cg43338979 | 360 | CATCATCTCCTG AAGATGCTAGC AC[C/T]GTTTCT GTTATATTCCAA CTCACTC | C | T | Thr | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O45933 Y43F4B.4 - CAENORHABDITIS ELEGANS, 363 aa. | 1.40E-53 | 18 |
| 713 | cg38450437 | 104 | GAATTGGTTCTG AGGAGTTTGG GA[G/A]CTTCTTT TACTGATGGACA GAAATC | G | A | Glu | Glu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43168 KIAA0443 - HOMO SAPIENS (HUMAN), 1395 aa. | 3.50E-52 | |
| 714 | cg38450437 | 47 | CCAGGGAAGT GCACAGCCAGA GAA[T/C]TGGTC TTGCAACTGCAT CCAGTGTG | T | C | Asn | Asn | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43168 KIAA0443 - HOMO SAPIENS (HUMAN), 1395 aa. | 3.50E-52 | |
| 715 | cg43314946 | 458 | CCTTCCGGATG ACTTCTCCGCA TC[C/T]TGCCCC AGCAGCTGGAC AGCATACA | C | T | Leu | Leu | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD37447 BAW - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 402 aa. | 1.60E-51 | 17 |
| 716 | cg44010070 | 320 | TCAAGCACTCG GACGGGACGCG CAC[T/C]TGCGC CAAGCTCTATGA CAAGAGCG | T | C | Thr | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O35775 SYNCOLLIN (SIP9) - Rattus norvegicus (Rat), 145 aa. | 6.40E-51 | |

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|-----|------------|-----|--|---|---|-----|-------------------|-------------------|--|-----------|--|
| 717 | cg39380052 | 563 | ACCTCATCACCC CGTACCATCAG AC[C/T]CTCGAC AAGTCACTGA GCGTTTTC | C | T | Thr | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCGINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa. | 1.30E-50 | |
| 718 | cg39380052 | 641 | GTCGTGGCATC GGCCCGACCTA CTC[T/C]GACAA GATCAATCGGAT GGTATTC | T | C | Ser | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCGINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa. | 1.30E-50 | |
| 719 | cg39380052 | 662 | ACTCTGACAAGA TCAATCGGATG GGT[C]ATTGCG GTCCAGGATCTT TTGACG | T | C | Gly | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCGINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa. | 1.30E-50 | |
| 720 | cg43329819 | 585 | TCATCGACAACC AGAACCTCCTCT TT[C]GAGCTCT CCTACAAGCTG GAGGCAA | T | C | Phe | SILENT- CODING | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa. | 1.40E-50 | |
| 721 | cg43298242 | 138 | CTGAAGATCTGT TGGCAGGGCTC AC[A/G]GAGACG GGGTGAGGGG AGAGATCG | A | G | Ser | SILENT- CODING | water_ch annel | Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa. | 1.30E-163 | |
| 722 | cg43298242 | 150 | TGGCAGGGCTC ACAGAGACGGG GGT[G/A]AGGGG AGAGATCGTGG GTTTCATGAG | G | A | Leu | SILENT- CODING | water_ch annel | Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa. | 1.30E-163 | |

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|-----|------------|------|---|---|---|-----|---------------|------------------|---------------------------|--|-----------|---------------|
| 723 | cg43970780 | 1501 | GGAGTTCTGGT TCTGGTAGATG GAA[G/A]CTTTCT CTTTCAACAGGT CCAGACA | G | A | Ala | Val (1096) | CONSERVATI VE | apoptosi s | Human Gene SWISSNEW-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa. pcis:SWISSPROT-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa. Human Gene Similar to SWISSPROT- ID:Q16864 VACUOLAR ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (V-ATPASE F SUBUNIT) (V- ATPASE 14 KD SUBUNIT) - HOMO SAPIENS (HUMAN), 119 aa. Human Gene SPTREMBL-ID:Q15065 OB-CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa. | 2.30E-212 | 11 |
| 724 | cg43957906 | 460 | GGAGTCCTTGG CGGCGTCATAT GGG[T/C]GCTCC TTGGAGGGGAT CTCCAGGAC | T | C | His | Arg (1097) | CONSERVATI VE | ATPase_ associat ed | Human Gene Similar to SWISSPROT- ID:Q16864 VACUOLAR ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (V-ATPASE F SUBUNIT) (V- ATPASE 14 KD SUBUNIT) - HOMO SAPIENS (HUMAN), 119 aa. Human Gene SPTREMBL-ID:Q15065 OB-CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa. | 2.20E-58 | 12 |
| 725 | cg43952088 | 2923 | TGAGGGGAGCG TCGCCGGCCGC GGA[G/A]CAGAT GCCGCGGGGC CGCTCGCAG | G | A | Ala | Val (1098) | CONSERVATI VE | cadherin | Human Gene SPTREMBL-ID:Q15065 OB-CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa. | 0.00E+00 | 16 |
| 726 | cg43956666 | 613 | ACTCCTGTTCTG GGGACAGTTTG GT[A/G]TTAAAC ACTTAAATATAG ATCCGG | A | G | Ile | Val (1099) | CONSERVATI VE | cadherin | Human Gene SWISSNEW-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa. pcis:SWISSPROT-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa. | 1.20E-167 | 3 (3q13.1) |

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| 727 | cg43942011 | 1327 | TTCCCCCATGTGA AACATCTGGCTT G[C/T]GACAGGT GATTTTTCACA GGTAGG | C | T | Arg | His (1100) | CONSERVATI VE | complem entcept | Human Gene Similar to TREMBLNEW-ID:E246058 COMPLEMENT RECEPTOR 2 - MUS MUSCULUS (MOUSE), 651 aa (fragment). | 1.10E-69 | 1 (1q32) |
| 728 | cg43973728 | 987 | TATGAACACCCC AGATCTGAAGAA G[T/C]TGCTGTT CTGAAACAGAA GTTGGAG | T | C | Val | Ala (1101) | CONSERVATI VE | cyclin | Human Gene SWISSPROT- ID:P51946 CYCLIN H (MO15- ASSOCIATED PROTEIN) (P37) (P34) - HOMO SAPIENS (HUMAN), 323 aa. | 2.60E-172 | 5 (5q13.3) |
| 729 | cg44017721 | 291 | TCCTGCTCCTCC GTGGCCTCCTTT G[G/A]CAGCGCT GGCCAAGCCCC GGGTCAG | G | A | Ala | Val (1102) | CONSERVATI VE | cytochro me | Human Gene Similar to SPTREMBL- ID:O00761 CYTOCHROME OXIDASE SUBUNIT VIA HEART ISOFORM PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3)) - HOMO SAPIENS (HUMAN), 97 aa. | 2.40E-52 | 22 |
| 730 | cg43273880 | 5428 | CAAAAAGAGAAA GACGACGTGAC TG[G/C]GGGTAA GAAACCATTTTCG TCCAGAG | G | C | Gly | Ala (1103) | CONSERVATI VE | dna_rna _bind | Human Gene SWISSPROT- ID:O14647 CHROMODOMAIN- HELICASE-DNA-BINDING PROTEIN 2 (CHD-2) - HOMO SAPIENS (HUMAN), 1739 aa. | 0.00E+00 | 15 |
| 731 | cg43992911 | 485 | GAAGAAGAACTT TTTTAAACTGAA C[A/G]ATAAAAG TGAAAAAGATAA GAAGGA | A | G | Asn | Asp (1104) | CONSERVATI VE | glycoprot ein | Human Gene SWISSPROT- ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P- GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa. | 0.00E+00 | 7 |
| 732 | cg41029366 | 890 | TGCGGCCACAA AGAGGACGCGG GCGT[C]GGTGT GCTCAGAGCAC CAGTCCTGG | T | C | Val | Ala (1105) | CONSERVATI VE | glycoprot ein | Human Gene SPTREMBL-ID:Q61003 T CELL SURFACE GLYCOPROTEIN CD6 - MUS MUSCULUS (MOUSE), 665 aa. | 1.00E-234 | 11 |

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| 733 | cg43931167 | 2546 | CGAGAACTGAA GAAAGCAAGAA CAGT/GJCCTAC AAATGGATGAAC TCAAATGT | T | G | Val | Gly (1106) | CONSERVATI VE | helicase | Human Gene SWISSPROT- ID:O14232 PUTATIVE HELICASE C6F12.16 IN CHROMOSOME I - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 1117 aa. | 3.30E-307 | 5 |
| 734 | cg43925670 | 2360 | AATCTGAATTTT GTCATACTCTTC T[C/T]TCATTTT AAATTAAGTTT AAATC | C | T | Arg | Lys (1107) | CONSERVATI VE | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcsl:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0.00E+00 | 1 |
| 735 | cg43925670 | 2474 | TAGAACAAATGTT CTTGATTTTTTT [C/G]CCATCTTTA CAGACATAAGT GAGCC | C | G | Gly | Ala (1108) | CONSERVATI VE | interfero n | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcsl:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0.00E+00 | 1 |

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|-----|------------|------|--|---|---|---------------|---------------|------------------|--------|---|-----------|----|
| 736 | cg43928549 | 4637 | AATTGGCACATC TTGGCGCGAAA GT[C/T]GTTCAC TCTGGGTCGCA CAAGGAG | C | T | Asp (1109) | Asn (1109) | CONSERVATI VE | kinase | Human Gene SWISSNEW-ID:O00329 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, DELTA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT DELTA) (PTDINS-3-KINASE P110) (PI3K) (P110DELTA) - HOMO SAPIENS (HUMAN), 1044 aa.lpcis:SWISSPROT-ID:O00329 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, DELTA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT DELTA) (PTDINS-3-KINASE P110) (PI3K) (P110DELTA) - HOMO SAPIENS (HUMAN), 1044 aa.lpcis:SPTREMBL- ID:O00329 PHOSPHOINOSITIDE 3- KINASE - HOMO SAPIENS (HUMAN), 1044 aa. | 0.00E+00 | |
| 737 | cg42703622 | 409 | GAAGAAGGAAT TTGGAGGTGGC CAC[A/G]TTAA GATGAAGTATTT GGAACAGT | A | G | Ile (1110) | Val (1110) | CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa. | 3.00E-187 | 12 |
| 738 | cg44131752 | 925 | CTCTGCGTGCT CGTCCCGAAGT GAC[C/G]TGCCT GGTCCGACAA GGACACTGA | C | G | Leu (1111) | Val (1111) | CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa. | 7.80E-173 | 16 |
| 739 | cg25143358 | 394 | CAGGTGGCCAT TCGGGCGGCTT CAA[G/T]TTTCGT GGTCATGCCCG CGGTTC | G | T | Leu (1112) | Ile (1112) | CONSERVATI VE | kinase | Human Gene Similar to SWISSPROT- ID:P46546 GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) - CORYNEBACTERIUM GLUTAMICUM, 369 aa. | 2.70E-51 | |

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| 740 | cg43105476 | 702 | GCGAAACCAAGT TCGGTCTTTCAA AT[C/T]GGGATT AGCACCTCTAA GTAGCAGT | C | T | Asp | Asn (1113) | CONSERVATI VE | kinase inhibitor | Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa. | 7.80E-86 | |
| 741 | cg38642684 | 290 | ATATTGCCCTAGT AATTTCTGATAA T[C/T]ATTAAAGG TATGTAAGTTGC TAGTA | C | T | Asp | Asn (1114) | CONSERVATI VE | nuclease | Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POLY PROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |
| 742 | cg39518465 | 864 | CACCTTCCTAAAG GAGATGAAGGA AG[C/T]CCTGGG CACCCCTGGCG CAGCCAAT | C | T | Ala | Val (1115) | CONSERVATI VE | oncogen e | Human Gene SWISSPROT- ID:P15498 VAV PROTO-ONCOGENE - HOMO SAPIENS (HUMAN), 846 aa. | 0.00E+00 | |
| 743 | cg43021380 | 176 | CAGCCGCCCGG GGGGCTGCAGC GCC[G/A]TTAGT GCCACACGGCTG TCTATTGTA | G | A | Val | Ile (1116) | CONSERVATI VE | phosphat ase | Human Gene SWISSPROT- ID:Q16849 PROTEIN-TYROSINE PHOSPHATASE N PRECURSOR (EC 3.1.3.48) (R-PTP-N) (PTP IA-2) (ISLET CELL ANTIGEN 512) (ICA 512) (ISLET CELL AUTOANTIGEN 3) - HOMO SAPIENS (HUMAN), 979 aa. | 0.00E+00 | 2 |
| 744 | cg39728924 | 365 | CAATTGTGGAG AAGAGTATTTTT AT[G/A]TCGCTA CTCAAGGACCA CTGCTGAG | G | A | Val | Ile (1117) | CONSERVATI VE | phosphat ase | Human Gene Similar to TREMBLNEW-ID:D1024666 PROTEIN-TYROSINE- PHOSPHATASE (EC 3.1.3.48) - MUS MUSCULUS (MOUSE), 426 aa. | 1.20E-64 | |

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| 745 | cg42710490 | 851 | CAACACAGCCTAT TGCGGGAAGAA AT[G/A]TCCAGG GTGGAATCCGT TTTGGGGA | G | A | Val | Ile (1118) | CONSERVATI VE | polymera se | Human Gene SWISSNEW-ID:O54888 DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT) - RATTUS NORVEGICUS (RAT), 1135 aa.lpcis:TREMBLNEW-ID:G2739048 RNA POLYMERASE I 127 KDA SUBUNIT - RATTUS NORVEGICUS (RAT), 1135 aa. | 8.90E-172 | |
| 746 | cg44001078 | 316 | GGTTATCAGGA ACTTGGGATCTT CA[C/T]GGATTT CCATCTTGTTCT TCATCCA | C | T | Arg | His (1119) | CONSERVATI VE | struct | Human Gene TREMBLNEW- ID:G2920823 CARDIAC MYOSIN BINDING PROTEIN-C - HOMO SAPIENS (HUMAN), 1274 aa. | 0.00E+00 | |
| 747 | cg43916919 | 1113 | AGGTAGGAGTC CCCCGAGAAGA AGA[C/T]GCCCT GGTTCTCTTGC GCCACAGGC | C | T | Val | Ile (1120) | CONSERVATI VE | struct | Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa.lpcis:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa. | 4.3E-188 | 2 (2cen) |
| 748 | cg42930605 | 463 | CAGCTCCTTGCT GGTCTTCTGCA CC[C/T]TCACCT CCATGTCGTACT TCTCCTC | C | T | Arg | Lys (1121) | CONSERVATI VE | struct | Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa. | 1E-92 | 11 (11p15.5) |
| 749 | cg36824552 | 230 | AAGACGAGCCG AGGCTTCACCTA CC[A/G]CCTGCA CTTCTGGCTCG GAAAGGAG | A | G | His | Arg (1122) | CONSERVATI VE | struct | Human Gene Similar to SWISSPROT- ID:Q28046 ADSEVERIN (SCINDERIN) (SC) - BOS TAURUS (BOVINE), 715 aa. | 4E-80 | |

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| 750 | cg42522566 | 377 | CAACATCATGAA CCAGCTCAGCC AC[G/A]TAAACTT GATCCAACCTTTA TGATGC | G | A | Val | Ile (1123) | CONSERVATI VE | struct | Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.17) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa. | 6E-55 | |
| 751 | cg42522566 | 509 | GTACCACCTCA CTGAGTTGGAT GTG[G/A]TCTTG TTCACGAGGCA GATCTGTGA | G | A | Val | Ile (1124) | CONSERVATI VE | struct | Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.17) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa. | 6E-55 | |
| 752 | cg42489842 | 481 | TGCAAGTGAATA TGCCAAATACTG CTT[A/C]AGAAATA TTAGGAGTTGCA GCTAC | T | A | Ser | Thr (1125) | CONSERVATI VE | tm7 | Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa. | 7.3E-106 | |
| 753 | cg43919398 | 2201 | GTTAGTCTCTGT GGTGTGCTTATA A[T/C]CATTTGG GGTCCAACATTG ACATTT | T | C | Ile | Val (1126) | CONSERVATI VE | transcript factor | Human Gene SWISSPROT- ID:Q14188 TRANSCRIPTION FACTOR DP-2 (E2F DIMERIZATION PARTNER 2) - HOMO SAPIENS (HUMAN), 385 aa. | 2.7E-202 | 3 |
| 754 | cg20612302 | 300 | ATGGAGGCGGC CCACATGGCGG CCA[C/G]CGCCA TCCTCAACCTGT CCACGCGC | C | G | Thr | Ser (1127) | CONSERVATI VE | transcript factor | Human Gene Similar to SPTREMBL- ID:O08996 MYELIN TRANSCRIPTION FACTOR 1-LIKE - MUS MUSCULUS (MOUSE), 1182 aa. | 1.7E-53 | |
| 755 | cg44928196 | 1474 | GGCTCTGTTCC ATGGGAAATTCA TA[G/A]ACACGG GTTTTCTTTAC CATTCTA | G | A | Asp | Asn (1128) | CONSERVATI VE | ubiquitin | Human Gene TREMBLNEW- ID:G2827198 UBIQUITIN PROTEIN LIGASE - MUS MUSCULUS (MOUSE), 854 aa. | 0 | |

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| 756 | cg43301812 | 3784 | GGCTGGTCCTT CTCCATGGCTG GGATTCGCTCT GCTGGCCTTGG TTTTGCCCG | T | C | His | Arg (1129) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa. | 0.00E+00 | 3 |
| 757 | cg43917191 | 2735 | GCTTCTCTTTTC ACATTGTATGTA TTCCTCAGGTGT TCTTGCAACTCC AAAAACA | C | T | Asp | Asn (1130) | CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment). | 0.00E+00 | 4 |
| 758 | cg43918356 | 2637 | GCTCATGTCATC TTCATCTAGAAA C[G/A]CCCTCAC GGAAATGGAATT GCTGCC | G | A | Ala | Val (1131) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment). | 0.00E+00 | 12 |
| 759 | cg43932090 | 1186 | TCCTTTCAAGCT TTCTTTATGTTG TTTCCTATTGCT TCATTTCTTGA AGGTC | T | C | Lys | Arg (1132) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment). | 0.00E+00 | |
| 760 | cg43950437 | 794 | AGCCAGAGGCT GGTACCTAGAA CCA[G/C]TGGAT GGTTCTTGGCT GATGGCGC | G | C | Thr | Ser (1133) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15021 ORF - HOMO SAPIENS (HUMAN), 1401 aa. | 0.00E+00 | 12 |
| 761 | cg42935995 | 743 | GCCTCGCTCCC CGTCTGAGAGC CTC[A/G]CGCCC TCCAGCCAGCC GTCACCTGCT | A | G | Val | Ala (1134) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa. | 1.00E-274 | |
| 762 | cg43971614 | 2578 | TCCATTGTAATC CAATCCCCCAT GG[A/G]CATAAG AAGAGTCTTTTC CATAAA | A | G | Val | Ala (1135) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 5.30E-253 | 5 |

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| 763 | cg43922856 | 1581 | CTTGAAATTTC AGTCACCCCTATT G[A/G]CAACTAA GGATTCTGTTGCT TGAAGC | A | G | Val | Ala (1136) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2.00E-237 | 12 (12q22) |
| 764 | cg43922856 | 1783 | CCACTTGTCCT TCAGTCTCAGTT A[T/C]TCCAGCTT GAGAAATAGCTCT GATTG | T | C | Ile | Val (1137) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2.00E-237 | 12 (12q22) |
| 765 | cg43955639 | 282 | GGCCGCGGG GGATAGCTGCC CAGG[C/G]TCAG GAGGCTCTTG GCTCCTGCCA | C | G | Ser | Thr (1138) | CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment). | 2.80E-215 | |
| 766 | cg41022625 | 1121 | CACGGCGTTCT GGATCGTCTTCT CC[A/G]TCATTC ACATCATCGCCA CCCTGCT | A | G | Ile | Val (1139) | CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa. | 2.00E-207 | 11 |
| 767 | cg43119894 | 1960 | TGAGCATAGCT CTGAGCTCTCTT TA[C/T]ACGGTC AGGGTCCACAT AATGCATT | C | T | Val | Ile (1140) | CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAA75235 LACTOSYL CERAMIDE ALPHA-2,3- SIALYLTRANSFERASE (EC 2.4.99.9) - MUS MUSCULUS (MOUSE), 387 aa. | 2.30E-190 | 2 |
| 768 | cg43303845 | 1109 | AGAACGAGAGA GGCTGGAGAGA CTG[C/G]AACGG GAGAGGCAAGA AAGGGAGCG | C | G | Gln | Glu (1141) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa. | 1.90E-138 | |
| 769 | cg44927166 | 531 | GTCCTTGTCTC CCAATCCCTTTG G[C/T]GTTCTCG TTCCTTATCCCT TTCCTCT | C | T | Arg | His (1142) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA74876 KIAA0853 PROTEIN - HOMO SAPIENS (HUMAN), 967 aa (fragment). | 3.70E-133 | 13 |

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| 770 | cg38059286 | 473 | AGCTGTATAGCT CCAGTGGTCCT GA[G/T]CTCCGC CGCTCCCTCTTC TCACTGA | G | T | Glu | Asp (1143) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD39906 FH1/FH2 DOMAIN-CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa. | 4.00E-129 | |
| 771 | cg29351416 | 333 | CTGCCAGCCCA GCCCATCCCC TGA[G/T]GACCT GGCTTGTCAT GGGCACCA | G | T | Glu | Asp (1144) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. | 3.20E-127 | |
| 772 | cg43960639 | 987 | CCATGTCTGGG AGAATGGGAGC CTC[A/C]TCGCC CACTTGAAAGTC AAAGTAGA | A | C | Asp | Glu (1145) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB0416 P24B PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 217 aa. | 9.00E-111 | |
| 773 | cg43325007 | 1098 | GTGGATATATGT GGCCTGCAGTA TG[G/A]CCACACA GCTTCTCCTGG AGGCTGCC | G | A | Ala | Val (1146) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa. | 4.80E-110 | 20 |
| 774 | cg42907145 | 853 | GCCACCTCCCA TAACCTTCTCAG CA[G/A]CATAGA CTGACTTGCCA CATCGAGG | G | A | Ala | Val (1147) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:P50461 LIM DOMAIN PROTEIN, CARDIAC (MUSCLE LIM PROTEIN) (CYSTEINE-RICH PROTEIN 3) (CRP3) (LIM-ONLY PROTEIN 4) - Homo sapiens (Human), 194 aa. | 1.10E-108 | 11 |
| 775 | cg43972159 | 1374 | AAGCCATTAGGT TCTCGGGCTGC TG[A/T]ACTGTTC GATTTGACTTT TCITTC | A | T | Ser | Thr (1148) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa. | 2.60E-102 | 7 (12q24.1) |

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| 776 | cg39512856 | 508 | CCAGGGCTGTGC CGTTCCACTTCT GAT/AJATTCCC CTCCCGGCGAT AACCAGGT | T | A | Tyr | Phe (1149) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 777 | cg28461713 | 584 | TCTGCAAAATTG CTCCTGGGCAT GG[G/A]CAGCTT GCAGCTGAAGT TGGTTGTA | G | A | Ala | Val (1150) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47710 ALPHA-S1 CASEIN PRECURSOR - Homo sapiens (Human), 185 aa. | 5.90E-96 | 4 (4q21.1) |
| 778 | cg43969092 | 361 | CGGCGCCCGTC ATCACGGATGT GCA[C/A]GTCCC CGTCGGTCAGC AGCAGCACA | C | A | Val | Leu (1151) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA74913 KIAA0890 PROTEIN - HOMO SAPIENS (HUMAN), 1194 aa. | 6.30E-89 | |
| 779 | cg42688841 | 487 | GGTCATAGTAT AAAGAAGGCTT GA[C/T]GACAAA CAGTCTCTTGCC ATGGTCC | C | T | Val | Ile (1152) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 | |
| 780 | cg39523553 | 603 | GACGCGTTGGT TCCCGACGAAG ACG[C/T]CCGAG CGGCCAAGTGG GCGGTGGCG | C | T | Ala | Val (1153) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 | |
| 781 | cg39523553 | 819 | ATGGACGTGGT GCGCAACAGCC CTC[A/G]CGGAG TGAAGGTCCAG ATGGCTCTT | A | G | His | Arg (1154) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 | |

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| 782 | cg39523553 | 857 | CCAGATGGCTC TTTCCGCCTGG CCC[G]/CJAGCTC GATCAGGCATC AAGTGCCT | G | C | Glu | Gln (1155) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 | |
| 783 | cg35933325 | 274 | AACCACAGAGA ATACAGTGACAA CA[A/T]AGAAAC AAAATGACCAAA TGCCACT | A | T | Phe | Tyr (1156) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA74845 KIAA0822 PROTEIN - HOMO SAPIENS (HUMAN), 1581 aa. | 2.40E-74 | |
| 784 | cg41677120 | 544 | GTTGTTTAACTT AAGCAATTTTT G[G]/A]ATAAAAG TGGATTGCAAG GATATGA | G | A | Asp | Asn (1157) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 1.10E-71 | 11 |
| 785 | cg43951096 | 2850 | AACATCAACAAT CGTTATTGGGTC TTT[C]TATTTTTG CTAGAAGAAAGTA TCTGG | T | C | Lys | Arg (1158) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2.00E-71 | 17 |
| 786 | cg42696021 | 444 | GCTGTGCCGCC TTCACAATGAAG TG[A/G]ACCGGA AGCTGGGCAAG CCTGATTT | A | G | Asn | Asp (1159) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa. | 1.40E-69 | |
| 787 | cg34243633 | 447 | GCTGGCACCGA CATAAGAACTTG TTT[C]TCCAGCT GGGAGCAGCA TGGCAAC | T | C | Lys | Arg (1160) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. | 1.30E-68 | |
| 788 | cg34243633 | 472 | TTCCAGCTGGG GAGCAGCATGG CAA[C/T]CAGTG TGCCCAAAAGC CCCAGAAAGG | C | T | Val | Ile (1161) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. | 1.30E-68 | |

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| 789 | cg43942922 | 268 | GTCCTCTGTCAA GACCCCTGAAA CA[G/A]TTGTCC CCACAGCCCT GAGCTCCA | G | A | Val | Ile (1162) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.30E-68 | |
| 790 | cg43942922 | 310 | TGAGCTCCAGC CTTCCACCTCCA CA[G/A]ACCCAGC CTGTCACCTCTG AGCCAC | G | A | Asp | Asn (1163) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa. | 2.30E-68 | |
| 791 | cg44938009 | 1139 | TTCTGTCAATGT GGTCCGTGCCA TG[A/G]TTGATAA CTGGGATGTCC TCTTCCA | A | G | Ile | Val (1164) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO- TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) - Homo sapiens (Human), 587 aa. | 5.80E-66 | X |
| 792 | cg39516123 | 631 | AGCCCTCAGGC GCGCCACAGAA CAG[T/G]GGGCA CCAACACTCCC CCTAGTCCT | T | G | Val | Gly (1165) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 5.10E-62 | |
| 793 | cg44921974 | 279 | GATTATGTCGCC GTTGAGTTCCG TC[A/G]CAGACT TGATGTTTTGA AAGTTGT | A | G | Val | Ala (1166) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P07148 FATTY ACID-BINDING PROTEIN, LIVER (L-FABP) - Homo sapiens (Human), 127 aa. | 1.6E-61 | 2 (4q28) |
| 794 | cg42731307 | 497 | AAGGCATTGAT GATCCGGTCCC CCA[G/C]TGGGT TGATGGCAAGTT CTGGAATC | G | C | Leu | Val (1167) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.60E-61 | |
| 795 | cg42731307 | 534 | CAAGTTCTGGAAT TCCTCTGGAAT C[T/G]TCCCGGC TGAGAGTCCCA TTCTCTC | T | G | Glu | Asp (1168) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.60E-61 | |

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| 796 | cg44015614 | 1330 | TCCACAACCTCT TCTGATGAGATG TTTCCTCCATTT CCATGTGTTTGT CCAAG | T | C | Asn | Asp (1169) | CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa. | 3.30E-54 | |
| 797 | cg43298242 | 143 | GATCTGTTGGC AGGGCTCACAG AGA[C/T]GGGG TGAGGGGAGAG ATCGTGGGT | C | T | Val | Ile (1170) | CONSERVATI VE | water_ch annel | Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa. | 1.3E-163 | |
| 798 | cg43299610 | 842 | CTCCCAAGTGCC CGCCCGACTAC CAC[C/T]ACATC CACACCGAGAT CTCCCGGGA | C | T | His | Tyr (1171) | NON- CONSERVATI VE | ATPase_ associat ed | Human Gene Homologous to SWISSPROT-ID:P39986 PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa. | 1.40E-109 | |
| 799 | cg42532480 | 564 | TTTCCTGAATGA ATGTTAAAGATT C[T/A]GTCAAGG TCAGTATGGCG ATCCAAG | T | A | Arg | End (1172) | NON- CONSERVATI VE | cadherin | Human Gene Homologous to SWISSPROT-ID:P79995 CADHERIN- 10 PRECURSOR - GALLUS GALLUS (CHICKEN), 789 aa.[pcls:SPTREMBL- ID:P79995 CADHERIN-10 - GALLUS GALLUS (CHICKEN), 789 aa. | 6.00E-115 | |
| 800 | cg42926989 | 259 | GCAATGAGCTG CTGGCAGCACAC AAG[G/T]CTTATC GCACCAGGAAA GATGCAGC | G | T | Ala | Asp (1173) | NON- CONSERVATI VE | cathepsi n | Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa. | 1.7E-136 (14q11.2) | 14 |
| 801 | cg43991318 | 2521 | TGGTCCGGGAA TACCTGGTGA CCC[T/G]GCGGG CCCGGCTGCCA GGAGCTGCC | T | G | Cys | Gly (1174) | NON- CONSERVATI VE | collagen | Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa. | 1.3E-73 1 (1p34) | |

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| 802 | cg43920512 | 1467 | AATTCAAAGTAT CATGGTGTTCCT CTTCJCCCTCAAC CCACCAGAGAC ACTAAAT | T | C | Leu | Pro (1175) | NON- CONSERVATI VE | cyclin | Human Gene SWISSPROT- ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa. | 4.1E-231 | 4 (4q27) |
| 803 | cg43063374 | 1763 | AGAGATTGAAC GTGTGGTTGGC AGA[A/C]ACCGG AGCCCCTGCT GCAGGACAG | A | C | Asn | His (1176) | NON- CONSERVATI VE | cyto450 | Human Gene SWISSNEW-ID:P33259 CYTOCHROME P450 2C17 (EC 1.14.14.1) (CYPIIC17) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa. pcls:SWISSPROT-ID:P33259 CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa. | 3.2E-254 | 10 (10q24.1) |
| 804 | cg21416244 | 360 | GGGTGAACGT CTATCCACCATT ATC/TJATCTATT CAGGCACATTC AGGACCT | C | T | Ser | Leu (1177) | NON- CONSERVATI VE | cytochrome | Human Gene Similar to SWISSPROT- ID:P98001 CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) - SACCHAROMYCES DOUGLASII (YEAST), 534 aa. | 5.5E-69 | |
| 805 | cg44017721 | 217 | AGATAGGAGTT GAAGGTGCAGA GGG[C/T]CACGC TGGGCAGCGCC AGCACGAAG | C | T | Ala | Thr (1178) | NON- CONSERVATI VE | cytochrome | Human Gene Similar to SPTREMBL- ID:O00761 CYTOCHROME OXIDASE SUBUNIT VIA HEART ISOFORM PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3)) - HOMO SAPIENS (HUMAN), 97 aa. | 2.4E-52 | 22 |
| 806 | cg43275625 | 1105 | TGGTACTCCCTT GCCGCCAGCTT GGJ[A/G]JTCATG GTACACGTTGG GTTTGGA | A | G | Ser | Pro (1179) | NON- CONSERVATI VE | deaminase | Human Gene SPTREMBL-ID:O00465 DSRNA ADENOSINE DEAMINASE DRADA2C - HOMO SAPIENS (HUMAN), 714 aa. | 0 | 21 |

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| 807 | cg43312829 | 1402 | TAGTGAATACT CCAATCAAAGAC A[A/G]CAGGACT CCATGTAACTGA ATATGA | A | G | Thr | Ala (1180) | NON- CONSERVATIVE | dehydrogenase | Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa. | 0 | 4 |
| 808 | cg43959136 | 1144 | TGGGCCAACAA GCTTGAGTGCG ATC[C/T]GGTCT GCAATGATGGA GGAATTGCC | C | T | Arg | Gln (1181) | NON- CONSERVATIVE | dehydrogenase | Human Gene SWISSPROT-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1- THF SYNTHASE) (METHYLENETETRAHYDROFOLAT E DEHYDROGENASE (EC 1.5.1.5) / METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYL TETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa. pcds:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLAT E DEHYDROGENASE (EC 1.5.1.5) / METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYL TETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa. | 0 | 14 |

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| 815 | cg39709402 | 57 | GATGCTGGAGG ACTTCAAGAAAG AC[A/G]TGAAGA ACTCCCTTAGAG AAACACA | A | G | Met | Val (1188) | NON- CONSERVATI VE | dna_rna _bind | Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment). | 3.20E-57 | |
| 816 | cg39709402 | 76 | AAAGACATGAA GAACTCCCTTAG AG[A/G]AACACA GGAAAACATTAA TAAACAA | A | G | Glu | Gly (1189) | NON- CONSERVATI VE | dna_rna _bind | Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment). | 3.20E-57 | |
| 817 | cg39709402 | 94 | CTTAGAGAAACA CAGGAAAACATT A[A/G]TAAACAA GTAGAAAGCCTA CAGAGAG | A | G | Asn | Ser (1190) | NON- CONSERVATI VE | dna_rna _bind | Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment). | 3.20E-57 | |
| 818 | cg39709402 | 96 | TAGAGAAACACA GGAAAACATTAA T[A/G]AACAAAGT AGAAGCCTACA GAGAGGA | A | G | Lys | Glu (1191) | NON- CONSERVATI VE | dna_rna _bind | Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment). | 3.20E-57 | 16 |
| 819 | cg43950268 | 1949 | TTTGCTATGTCC TCCTTGACCTCC T[G/A]CTCGGTG GCGGTCACAAT GCCCTCC | G | A | Gln | End (1192) | NON- CONSERVATI VE | eph | Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa. | 0.00E+00 | |
| 820 | cg43985169 | 540 | AAGACGAATGG GTGGTGGTAGA GATT[C]CTGAA GAAATGGAAATA GATGGTGA | T | C | Ser | Pro (1193) | NON- CONSERVATI VE | eph | Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa. | 2.40E-123 | |
| 821 | cg43997616 | 2250 | AAAGCCAGCGG AGCCGTAAGCA TCAIT/CJACTGCT TCCTCTTCACCT CATCACT | T | C | Tyr | Cys (1194) | NON- CONSERVATI VE | eph | Human Gene Similar to TREMBLNEW-ID:G2735762 HEAT SHOCK PROTEIN DNAJ - LEPTOSPIRA INTERROGANS, 369 aa. | 1.40E-55 | |

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| 822 | cg43319420 | 992 | CACGACAACTA CAGAAACAACC CCTT/CJCCACA ACTTCCGGCAC TGCTTCTGC | T | C | Phe | Ser (1195) | NON- CONSERVATI VE | esterase | Human Gene Similar to SWISSNEW- ID:Q23917 3',5'-CYCLIC- NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. pcls:SWISSPROT-ID:Q23917 3',5'- CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. | 3.30E-60 | 21 |
| 823 | cg44034764 | 382 | GAGGTCCAGGC TGGGCAGGACA GTC/T/CJCCCCA TGGTGCCGTA CAGCCTCTT | T | C | Glu | Gly (1196) | NON- CONSERVATI VE | glycoprotein | Human Gene SWISSPROT- ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa. | 0.00E+00 | 7 (Xp21.2) |
| 824 | cg43991224 | 217 | TCTCATCTGTCT ACCTACAGCCT GGT/AJTTGGGT CATGGCAGCAG TGGTGCTG | T | A | Val | Asp (1197) | NON- CONSERVATI VE | glycoprotein | Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa (fragment). | 1.50E-139 | |
| 825 | cg44018623 | 1824 | TACCATCTCTGT TTTTACCACTGG T[G/A]GCTCTGA ACAACAAATAAT TTGTGG | G | A | Pro | Leu (1198) | NON- CONSERVATI VE | glycoprotein | Human Gene Homologous to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa. | 1.90E-114 | 6 |
| 826 | cg38924741 | 598 | AAAGAGGAGAA TGGTGACTTTGC CTT/CJATTCAGA GTGGAACGAGC TGAAAGG | T | C | Leu | Ser (1199) | NON- CONSERVATI VE | glycoprotein | Human Gene Similar to SWISSPROT- ID:P04196 HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG) - HOMO SAPIENS (HUMAN), 525 aa. | 3.30E-55 | |

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| 827 | cg43322513 | 13082 | TTCCTGTTCTTC ACATGGTGAGC CC[C/T]GCCCTG CTGTCTGCTTGC ATTCGGG | C | T | Arg | Gln (1200) | NON- CONSERVATIVE | glycoprotein | Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE- RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa. | 3.30E-54 | 12 |
| 828 | cg44913214 | 2306 | GAACACAAACAA GAAAAAACAGA GT[C/T]TGGGAC TCATCCAAAAGG GACGAGA | C | T | Ser | Phe (1201) | NON- CONSERVATIVE | helicase | Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa. | 0.00E+00 | 10 |
| 829 | cg39529972 | 278 | TGGCCCTCGAC ATCATTCCTGA CG[A/G]GGACTT AAAGGGTAGCA ATTCGTAT | A | G | Ser | Pro (1202) | NON- CONSERVATIVE | hydrolase | Human Gene Similar to SWISSPROT- ID:Q01477 UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 3 (EC 3.1.2.15) (UBIQUITIN- THIOLESTERASE 3) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 3) (DEUBIQUITINATING ENZYME 3) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 912 aa. | 1.00E-52 | |
| 830 | cg43925670 | 2309 | TAGTTTGCCCAA ACCAGCATCAC CT[C/G]GGAAC TTTCTTCCATCA AGTCAGC | C | G | Arg | Pro (1203) | NON- CONSERVATIVE | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. ipclis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0.00E+00 | 1 |

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| 831 | cg43925670 | 2369 | TTTGTCACTC TTCTCTCATTT T/A/G/AATTAAAGT TTTAAATCGTTG CTCAG | A | G | Leu | Ser (1204) | NON- CONSERVATIVE | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.pcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0.00E+00 | 1 |
| 832 | cg43925670 | 2458 | CCTCTAATCCTT TTAGTAGAACAA T[G/T]TTCCTGTA TTTTTTTCCCAT CTTTA | G | T | Asn | Lys (1205) | NON- CONSERVATIVE | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.pcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0.00E+00 | 1 |
| 833 | cg43925670 | 2467 | CTTTTAGTAGAA CAATGTTCTTGT A[T/G]TTTTTTTCC CATCTTTACAGA CATAA | T | G | Lys | Asn (1206) | NON- CONSERVATIVE | interferon | Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.pcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment). | 0.00E+00 | 1 |

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| 834 | cg43331742 | 845 | TCCTCGAGGTG CTTCCCACAGA CTC[G/A]ATTTCT GAGTTTCCACA GAAAAGA | G | A | Ser | Leu (1207) | NON- CONSERVATI VE | isomerase | Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-) - RATTUS NORVEGICUS (RAT), 361 aa. | 5.60E-131 | |
| 835 | cg43253796 | 1812 | GAAATGGATCTT ATTGGACTTTG C[G/T]ACAAGAC TGCCGAGAGAT TTTCCCA | G | T | Arg | Leu (1208) | NON- CONSERVATI VE | kinase | Human Gene SWISSNEW-ID:P42338 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137) (PI3- KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1070 aa. pcds:SWISSPROT-ID:P42338 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137) (PI3- KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1070 aa. | 0.00E+00 | |
| 836 | cg43257400 | 2094 | GACATCAGCAT GGCTGCCCCCG ACTT[C]CAGCA GAACATGATCAT TCTCTGAC | T | C | Ser | Pro (1209) | NON- CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa. | 0.00E+00 | 10 |
| 837 | cg43974480 | 686 | TCACGGACTTTG GACTGTCCAAA T[G/T]GGCCTCA TGAGCCTGACA ACGAACT | G | T | Met | Ile (1210) | NON- CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:O00114 HYPOTHETICAL HUMAN SERINE- THREONINE PROTEIN KINASE R31240_1 - HOMO SAPIENS (HUMAN), 1237 aa (fragment). | 0.00E+00 | |
| 838 | cg43922705 | 4337 | CAAACCGGCTTT CTCCATGGTGC CC[T/C]GCCAAA CCCTGGAGTTC CCAGGCTG | T | C | Gln | Arg (1211) | NON- CONSERVATI VE | kinase | Human Gene SWISSPROT- ID:P27987 1D-MYO-INOSITOL- TRISPHOSPHATE 3-KINASE B (EC 2.7.1.127) (INOSITOL 1,4,5- TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 505 aa (fragment). | 3.80E-279 | 1 (1q41) |

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| 839 | cg38438124 | 1460 | TGCAAAAACTGT TAAACATGGCG CT[G/C]GCGCGG AGATCTCCACC GTGAACCC | G | C | Gly | Arg (1212) | NON- CONSERVATI VE | kinase | Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa. | 2.80E-216 | 10 |
| 840 | cg42703622 | 385 | GTATGCAGCAA CAAGAGCAACT CTG[A/G]AGAAG GAATTTGGAGG TGGCCACAT | A | G | Lys | Glu (1213) | NON- CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa. | 3.00E-187 | 12 |
| 841 | cg42703622 | 395 | ACAAGAGCAAC TCTGAAGAAGG AAT[T/C]TGGAG GTGCCACATT AAAGATGAA | T | C | Phe | Ser (1214) | NON- CONSERVATI VE | kinase | Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa. | 3.00E-187 | 12 |
| 842 | cg41501665 | 96 | GAGTACACCAT CAAGTCGCACT CCA[G/A]CTTGC CGCCCAACAAC AGCTACGCC | G | A | Ser | Asn (1215) | NON- CONSERVATI VE | kinase | Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.70E-76 | |
| 843 | cg25143358 | 457 | GCTTTATGGTA TCGACATCCAAT G[C/T]GTCGATG TCCTCCACAACC TCCACG | C | T | Ala | Thr (1216) | NON- CONSERVATI VE | kinase | Human Gene Similar to SWISSPROT- ID:P46546 GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) - CORYNEBACTERIUM GLUTAMICUM, 369 aa. | 2.70E-51 | |
| 844 | cg29023997 | 179 | TGCATGGTTTCC ATTTCAACTCTG G[A/G]TGGGATG GAGCACCATGT GCGCACC | A | G | Asp | Gly (1217) | NON- CONSERVATI VE | kinasere ceptor | Human Gene SWISSPROT- ID:P36896 SERINE/THREONINE- PROTEIN KINASE RECEPTOR R2 PRECURSOR (EC 2.7.1.37) (SKR2) (ACTIVIN RECEPTOR-LIKE KINASE 4) (ALK-4) (ACTR-IB) - HOMO SAPIENS (HUMAN), 505 aa. | 9.30E-280 | 12 |

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| 845 | cg43975720 | 3917 | CATCCACCCAG CCCAAGATGAC CGG[A/C]CCTTT TACCAATTTGAG GCTGCGTG | A | C | Thr | Pro (1218) | NON- CONSERVATI VE | kinesin | Human Gene SWISSPROT- ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa. | 0.00E+00 | 2 |
| 846 | cg44013875 | 1710 | GCCATGGAGAG GCTGCAGGAGA CAG[A/G]GAAGA TTATAGCTGAGC TGAAACGAG | A | G | Glu | Gly (1219) | NON- CONSERVATI VE | kinesin | Human Gene SWISSNEW-ID:Q43896 KINESIN-LIKE PROTEIN KIF1C - HOMO SAPIENS (HUMAN), 1103 aa. pcds:TREMBLNEW-ID:G2738149 KINESIN-LIKE MOTOR PROTEIN KIF1C - HOMO SAPIENS (HUMAN), 1103 aa. | 0.00E+00 | |
| 847 | cg44009224 | 2806 | TTTGGATCCTGA AAATGTTGTATT TTT[C/J]ATGTTGGA GGTTACCCACC TGATTT | T | C | Tyr | His (1220) | NON- CONSERVATI VE | laminin | Human Gene SWISSPROT- ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa. | 0.00E+00 | |
| 848 | cg42930646 | 1228 | TGATGCGGATA GCGTATGGATG GAA[A/G]TGGAC GATGAGGAGGA CCTGCCTTC | A | G | Met | Val (1221) | NON- CONSERVATI VE | laminin | Human Gene SWISSPROT- ID:P07221 CALSEQUESTIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ-BINDING PROTEIN) - ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa. | 1.80E-198 | 1 |
| 849 | cg43935885 | 3745 | CCAGACAGCAC CACTGGAACCC CTC[C/T]TAGCA GCGCACCCAGAC CCGAAGAAC | C | T | Pro | Leu (1222) | NON- CONSERVATI VE | MHC | Human Gene SPTREMBL-ID:P79457 MALE-SPECIFIC HISTOCOMPATIBILITY ANTIGEN H- YDB - MUS MUSCULUS (MOUSE), 1186 aa. | 7.20E-173 | |
| 850 | cg42928872 | 1807 | GAGCTGCAGAG GAGGCTGGACC AGT[C/T]CATTG GGAAGCCCTCA CTGTTCATC | C | T | Ser | Phe (1223) | NON- CONSERVATI VE | misc_ch annel | Human Gene TREMBLNEW- ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa. | 0.00E+00 | 11 |

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| 851 | cg44019843 | 929 | GAGTGACCCGC CTCCCTGGTCC AAGATATGTG GAGTACACCTTC ACAGGGAT | A | T | Asn | Tyr (1224) | NON- CONSERVATI VE | misc_ch annel | Human Gene SPTREMBL-ID:Q15478 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1836 aa. | 0.00E+00 | 17 (17q23.1) |
| 852 | cg44128805 | 1396 | AGTGCACACAG TGAGCTCAGAG CTT[C/T]CCCC GAAACCGAAA GTTTCAACT | C | T | Glu | Lys (1225) | NON- CONSERVATI VE | nuclease | Human Gene Similar to SWISSPROT- ID:P54278 PMS1 PROTEIN HOMOLOG 2 (DNA MISMATCH REPAIR PROTEIN PMS2) - HOMO SAPIENS (HUMAN), 862 aa. | 1.60E-76 | 7 |
| 853 | cg38642684 | 304 | TTTCTGATAATC ATTAAAGGTATG TATATAGTTGCTA GTATTTAATTTA ACCTT | A | T | Leu | End (1226) | NON- CONSERVATI VE | nuclease | Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcsl:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |
| 854 | cg38642684 | 417 | CTTTTCAGGTG CAATGATTAAAC C[AT]CTTAACTG TGCATTCCTTAT GACAG | A | T | Ser | Arg (1227) | NON- CONSERVATI VE | nuclease | Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcsl:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa. | 2.60E-50 | |

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| 855 | cg44913844 | 1194 | CCAGTTGGTAAA CTGGTCTTAAAC C[G/A]GAATCCA GTTAATTACTTT GCTGAG | A | Arg | Gln (1228) | NON- CONSERVATI VE | peroxidase | Human Gene SWISSPROT- ID:P04040 CATALASE (EC 1.11.1.6) - HOMO SAPIENS (HUMAN), 527 aa. | 2.70E-296 | 11 (11p13) |
| 856 | cg40084915 | 5005 | TCTGCGGTCTG GGGAGATGAGG GCC[T/C]CAAAC AGCACCTGATAT TCATTGGG | C | Glu | Gly (1229) | NON- CONSERVATI VE | phosphatase | Human Gene SPTREMBL-ID:O00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR - HOMO SAPIENS (HUMAN), 1436 aa. | 0.00E+00 | 1 |
| 857 | cg42720088 | 214 | AAAGCTCAGAG AGATCTGGGCT ATG[A/T]GCCAC TTGTCAGCTGG GAGGAAGCC | T | Glu | Val (1230) | NON- CONSERVATI VE | reductase | Human Gene Similar to SWISSPROT- ID:P22072 3 BETA- HYDROXYSTEROID DEHYDROGENASE/DELTA 5->4- ISOMERASE TYPE II (3BETA-HSD II) (3-BETA-HYDROXY-DELTA(5)- STEROID DEHYDROGENASE (EC 1.1.1.145) (3-BETA-HYDROXY-5- ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE) / STEROID DELTA-ISOMERASE (EC 5.3.3.1) (DELTA-5-3-KETOSTEROID ISOMERASE)) - RATTUS NORVEGICUS (RAT), 372 aa. | 2.40E-50 | |
| 858 | cg43957486 | 1528 | CGCTCCTGCAC CGCATCCGCGA CGC[A/T]GTCCT GCAACGACCTC TGCGAGCAC | T | Gln | Leu (1231) | NON- CONSERVATI VE | struct | Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa. | 0.00E+00 | 20 (20p11.2) |
| 859 | cg40148056 | 1462 | CTCAGAGACCC CTAACAAACCCA GCA[G/C]CCACA GAGCGGAACAC TTAAGGATC | C | Gln | His (1232) | NON- CONSERVATI VE | struct | Human Gene SPTREMBL-ID:Q92777 SYNAPSIN IIB - HOMO SAPIENS (HUMAN), 478 aa. | 2.90E-260 | 3 (3p) |

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| 863 | cg43297806 | 994 | TGCAGGGAGCG TAGTGCCAGAG GGG[T/C]CTGGG AGGAGGCTGAA ATCACCTGA | T | C | Thr | Ala (1236) | NON- CONSERVATI VE | sulfotran sferase | Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.jpcls:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883.aa | 0.00E+00 | 10 |
| 864 | cg43987111 | 1337 | AGTAGTCTGCG TCTCCATAGAGT TT[C/A]CTCATGA CTGAGTTCCTGG TCTGGA | C | A | Arg | Ser (1237) | NON- CONSERVATI VE | synthase | Human Gene SWISSPROT- ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa. | 0.00E+00 | 18 (1p34.1) |
| 865 | cg43976335 | 633 | GAAATGCACTG GACCACTCGGG CAG[G/A]GCTGC CAGGCCGTAGC AGGCAATTC | G | A | Pro | Ser (1238) | NON- CONSERVATI VE | synthase | Human Gene SWISSPROT- ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa. | 5.30E-240 (20q11.2) | 20 |
| 866 | cg39515668 | 605 | ACGCACGAACC GGTCATACTGG TCG[G/T]TGATC CAGGAACGGTC GCACAGCTG | G | T | Thr | Asn (1239) | NON- CONSERVATI VE | synthase | Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa. | 2.80E-72 | |
| 867 | cg44027791 | 1261 | GAAGCGCTTCT GACACTGGGCG CAC[T/C]CGAAG CGTTGTCCCTT GTGTGGGT | T | C | Glu | Gly (1240) | NON- CONSERVATI VE | transcript factor | Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa. | 0.00E+00 | 17 |

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| 868 | cg43992817 | 578 | GAGGGGCCGCT GGAAGGTGACA CTG[C/T]GTTGG GGCCACGGAG GTGCCGCTG | C | T | Ala | Thr (1241) | NON- CONSERVATIVE | transcript factor | Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY- LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa. | 1.50E-144 | 3 |
| 869 | cg43297259 | 816 | TAAGTGCTCTGAT GAGGTGIGACT TC[T/C]GGCTAA AGCCTTGCTCA CACTCCCT | T | C | Gln | Arg (1242) | NON- CONSERVATIVE | transcript factor | Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcsl:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. | 7.80E-54 | |
| 870 | cg42716761 | 1594 | CGAGAAAGACCC TATACCATCACG TG[C/G]ACGGCT GCGACGTGTC CACCTCCG | C | G | His | Asp (1243) | NON- CONSERVATIVE | transcript factor | Human Gene SWISSNEW-ID:Q61079 SINGLE-MINDED HOMOLOG 2 (SIM TRANSCRIPTION FACTOR) (MSIM) - MUS MUSCULUS (MOUSE), 657 aa. pcsl:SWISSPROT-ID:Q61079 SINGLE-MINDED HOMOLOG 2 (SIM TRANSCRIPTION FACTOR) (MSIM) - MUS MUSCULUS (MOUSE), 657 aa. | 5.7e-312 | 21 |
| 871 | cg42166807 | 2828 | AGAGCAATGGC TCTCTTCACTCC GT[G/A]GAAGTT GTCCTCTCAGAA GCTGGGC | G | A | Trp | End (1244) | NON- CONSERVATIVE | transferase | Human Gene SWISSPROT- ID:Q09328 ALPHA-1,3(6)- MANNOSYLGLYCOPROTEIN BETA- 1,6-N-ACETYL- GLUCOSAMINYLTRANSFERASE V (EC 2.4.1.155) (ALPHA-MANNOSIDE BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFE RASE) (N-ACETYLGLUCOSAMINYL- TRANSFERASE V) (GNT-V) (GLCNAC-T V) - HOMO SAPIENS (HUMAN), 741 aa. | 0.00E+00 | 2 (2q21) |

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| 872 | cg38869466 | 752 | TTCACCTGTATT AACGTCCTGGT CCGTCGGGCTT CATAATGGTGTC AGGATTT | T | C | Leu | Pro (1245) | NON- CONSERVATI VE | transport | Human Gene SWISSPROT- ID:P30825 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG) - HOMO SAPIENS (HUMAN), 629 aa. | 0.00E+00 | 13 |
| 873 | cg42742340 | 3392 | CAGAGAGACGG TGTCATCAGCA TCGTCGGCCT CCCTGCAGCAG ACCCAGGC | C | T | Arg | Trp (1246) | NON- CONSERVATI VE | transport | Human Gene SWISSPROT- ID:Q04671 P PROTEIN (MELANOCYTE-SPECIFIC TRANSPORTER PROTEIN) - HOMO SAPIENS (HUMAN), 838 aa. | 0.00E+00 | 15 |
| 874 | cg43976701 | 513 | TGGTATATCTGA ACTGAATCAGC CTGTCCTGAAC TTTTACCTCAGT TTTCTAG | G | C | Ala | Pro (1247) | NON- CONSERVATI VE | transport | Human Gene SWISSPROT- ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa. | 0.00E+00 | |
| 875 | cg43920728 | 2024 | GTAAGTCTCATT GTAAATTTGTTG C[A/G]TGAGCAG TGCTGGGGAGT TGACAGC | A | G | Cys | Arg (1248) | NON- CONSERVATI VE | transport | Human Gene SWISSPROT- ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa. | 2.90E-237 | 1 (1p31) |
| 876 | cg43920728 | 2185 | TGCTTGCTCTG GAAGGGCAGAG TGCTCTGCTCA CCTCCTTTTAGC CAAAGTAA | C | T | Arg | Gln (1249) | NON- CONSERVATI VE | transport | Human Gene SWISSPROT- ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa. | 2.90E-237 | 1 (1p31) |

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| 877 | cg42339179 | 450 | TCCTCCACCAG GGTCATTTGCG GT[G/A]TTTAAAA GTTCCAGTGATC TCAATG | G | A | His | Tyr (1250) | NON- CONSERVATI VE | transport | Human Gene Homologous to SWISSNEW-ID:Q60714 LONG- CHAIN FATTY ACID TRANSPORT PROTEIN (FATP) - MUS MUSCULUS (MOUSE), 646 aa. pcis:SWISSPROT- ID:Q60714 LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP) - MUS MUSCULUS (MOUSE), 646 aa. | 1.90E+05 | 15 |
| 878 | cg17663981 | 383 | TGCACCTGCGA CCAAAAACCCCT GCA[G/A]CTGCC CCAAAGGGGAT GTCAACTAC | G | A | Ser | Asn (1251) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa. | 0.00E+00 | 10 (10p11.2 3) |
| 879 | cg43918356 | 1806 | GCTCCCTGTGCA CGGGGCTGTAG CGC[C/T]CAGGA CTGCCACAGGCC TGGCTTTGC | C | T | Gly | Glu (1252) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment). | 0.00E+00 | 12 |
| 880 | cg43924089 | 1080 | ACCTCCTGGAG CAGTCCTGGTG TTA[C/T]ATTCCC TGCCCTGGAG TTCCCACT | C | T | His | Tyr (1253) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA31589 KIAA0614 PROTEIN - HOMO SAPIENS (HUMAN), 1630 aa (fragment). | 0.00E+00 | 12 |
| 881 | cg43930961 | 2459 | TTCTCCGTAGT CACAGACGTTA GG[C/T]TACTGC TTTCGGCTTCAA TGGAAAC | C | T | Ser | Asn (1254) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa. | 0.00E+00 | 4 |
| 882 | cg43966528 | 680 | AACAACACATTC AGTACAGTGCA GC[A/G]TATCAG CAGGCCAAGTT AACCAATC | A | G | Met | Thr (1255) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O00237 HKF-1 - HOMO SAPIENS (HUMAN), 685 aa. | 0.00E+00 | |

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| 883 | cg43980727 | 1367 | TCCTCCTTGTA GTCAGAGACAT CA[G/A]GAGAGT AACTGGATGTTA GCTCCAA | G | A | Pro | Leu (1256) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa. | 0.00E+00 | 17 |
| 884 | cg43981483 | 1540 | TGACTGCATTAT TCGCAGCTGCT TA[A/G]GGACAA ATTCTACCTTCT TCTGGGT | A | G | Leu | Pro (1257) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75882 ATTRACTIN - HOMO SAPIENS (HUMAN), 1198 aa. | 0.00E+00 | 20 |
| 885 | cg44932392 | 1200 | TAGATGAAGGA GCCTGAGTAAG AGG[C/T]CACGC ACCAGCCTGTA GAACATATA | C | T | Trp | End (1258) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa. | 0.00E+00 | |
| 886 | cg44932924 | 2754 | AACAGTGAGTC GGTCAGCAGC AGA[T/C]GGAGT TCTTGAACAGG CAGCTGTG | T | C | Met | Thr (1259) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92574 HAMARTIN (MYELOBLAST KIAA0243) - HOMO SAPIENS (HUMAN), 1164 aa. | 0.00E+00 | 9 |
| 887 | cg43985955 | 2082 | ACCTCAAACC CCTTTGGCCCT GTA[T/C]CAGGA GCACAGATACA GTTTAAGTA | T | C | Ser | Pro (1260) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 2.70E-299 | |
| 888 | cg44002507 | 1373 | GTCGCACTTGG CAGCCAGCAGG ATC[C/T]CGGCT ATGTCACGCA GCCGGAGAA | C | T | Gly | Glu (1261) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa. | 8.10E-298 | |
| 889 | cg44002507 | 2870 | TTTCCTTTCCTC TTGAGAAATTC T[T/C]CTTAATGC TGGATTCCGAA CTCAGG | T | C | Lys | Glu (1262) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa. | 8.10E-298 | |

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| 890 | cg44002507 | 507 | CGCAGGTCCTG GTGGGCCATGA ACA[C/T]GCGCA CGGGCACCAGG TTGGGCTCG | C | T | Val | Met (1263) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa. | 8.10E-298 | |
| 891 | cg44128920 | 1086 | GAGCAGCAGCG AAAACGGCTTCA AC[A/C]GCAGTT GGAAGAACGCA GTCGTGAA | A | C | Gln | Pro (1264) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa. | 1.00E-290 | 19 |
| 892 | cg43968641 | 3315 | TCATTCATCTCA GGGAACATATC AG[C/T]CAGAGA AATATACAAGAA CATTCTCT | C | T | Ala | Thr (1265) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment). | 2.00E-285 | 8 |
| 893 | cg43934178 | 2180 | ACAAAGTAGTG GAACTTCCCTTT GA[A/G]CACGTC CAGGGTGTGGC CCAGGACC | A | G | Phe | Leu (1266) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD29670 DNA TOPOISOMERASE III BETA - HOMO SAPIENS (HUMAN), 862 aa. | 1.80E-274 | |
| 894 | cg43934178 | 2596 | CCAGGGCATGA CCTCCGTGAAG CCT[G/A]GTGAG AGGACGGTCTT CCCGGAGCA | G | A | Pro | Leu (1267) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD29670 DNA TOPOISOMERASE III BETA - HOMO SAPIENS (HUMAN), 862 aa. | 1.80E-274 | |
| 895 | cg43949042 | 378 | GGACGTACATG AGGACGGCTAT TGG[C/A]TGTC GATGATGAGCG ACAGCCACA | C | A | Gln | His (1268) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75907 ACAT RELATED GENE PRODUCT 1 - HOMO SAPIENS (HUMAN), 488 aa. | 6.10E-268 | |
| 896 | cg43916582 | 2097 | CCTTCATCTTTA TTCTGCTGCTCA GT[G/T]TCCATTT GTTCTCTCTTGAT TGGCT | T | G | Thr | Pro (1269) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75475 LENS EPITHELIUM- DERIVED GROWTH FACTOR - HOMO SAPIENS (HUMAN), 530 aa. | 2.30E-259 | |

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| 897 | cg43258841 | 485 | AACTCCATCCAC AAGTCCCTTGCTG A[A/G]TAATCAAT CGCTGAGCCTC ATCTCT | A | G | Ile (1270) | Thr (1270) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa. | 2.70E-258 | |
| 898 | cg43979679 | 619 | GAGAAAGGAGCC CGGAAAGTGT GAC[C/T]AGGAG AAACCGGCACC CAGCTTTGC | C | T | Gln (1271) | End (1271) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q13977 MAJOR YO PARANEOPLASTIC ANTIGEN - HOMO SAPIENS (HUMAN), 509 aa (fragment). | 5.60E-258 | 16 (16p13.1) |
| 899 | cg42202923 | 887 | TACCCCAATGGT CTTCAGCCTCTG C[A/G]GCAGCTC CGATGAGGTCA GCTGCCG | A | G | Leu (1272) | Pro (1272) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75926 PROTEIN INHIBITOR OF ACTIVATED STAT PROTEIN PIASY - HOMO SAPIENS (HUMAN), 510 aa. | 2.40E-256 | |
| 900 | cg43320405 | 994 | CCAGGCCCTCGA ATGGACAGCAC CTT[C/A]ATGATG GGTCTGTGGTG GCTCAGGC | C | A | Met (1273) | Ile (1273) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:CAB4624 DKFZP434G153 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa. | 8.20E-245 | |
| 901 | cg43917689 | 3689 | TGACAACGCAG GCTCCAGGGGT TGT[G/A]GCTGA TCTTCTCAGAAC TCAAGCCA | G | A | His (1274) | Tyr (1274) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa. | 3.50E-240 | 3 |
| 902 | cg43922856 | 1546 | GAGAATTCAGT GATTGGCAGAA TAG[G/A]AGATG CATGCTTGAAT TTCCAGTC | G | A | Pro (1275) | Ser (1275) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2.00E-237 | 12 (12q22) |
| 903 | cg43922856 | 1608 | AACTAAGGATTCA GTTGCTTGAAG CC[A/T]TTATAGT TTCAGCTATGG GAGTACT | A | T | Met (1276) | Lys (1276) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa. | 2.00E-237 | 12 (12q22) |

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| 911 | cg43996402 | 684 | CTTCTCCGGCT CCTTTCCTCCCT GC[C/A]GTGGCT TCTGCTGCTCC CCTCCCTT | C | A | Gly | Cys (1284) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q12804 RECEPTIN - HOMO SAPIENS (HUMAN), 451 aa. | 2.60E-189 | 2 |
| 912 | cg43984909 | 1268 | CGAATATCAGCT GCATCCAGTGT CC[C/T]CAGACG AGAATACAAGC CAAGGCCT | C | T | Pro | Leu (1285) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q99963 PROTEIN CONTAINING SH3 DOMAIN, SH3GL3 - HOMO SAPIENS (HUMAN), 347 aa. | 1.70E-187 | 15 |
| 913 | cg42910688 | 778 | GACAGAGGACA TTCCCATAAATT TG[G/T]TTGGCA ACAAAAGTGACT TAGTGCG | G | T | Val | Phe (1286) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P55040 GTP-BINDING PROTEIN GEM (GTP-BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa. | 7.70E-158 | 8 |
| 914 | cg43950590 | 1351 | AAGAACTCCTCC GACGGCTTCGT TAC[C/T]ATCCTG TCTGAAGCGGA TTGCACGA | C | T | Gly | Ser (1287) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa. | 1.90E-154 | 7 |
| 915 | cg44931503 | 945 | TTTTAAAGAGTT CATATAATCATA G[A/G]GGTCTTC AAATACCGTTGT TCCTTC | A | G | Leu | Pro (1288) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD34078 CGI-83 PROTEIN - HOMO SAPIENS (HUMAN), 288 aa. | 5.00E-154 | |
| 916 | cg43303845 | 774 | ACATTGCCTAGA CAAAACTCACAA C[T/C]ACCTGCT CAAGTTCAAAAT GGCCCA | T | C | Leu | Pro (1289) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa. | 1.90E-138 | |
| 917 | cg43973762 | 117 | AGCTGAACAAC AGAAATTGTGG AAT[G/T]AGGAG TTAAAATATGCC AGAGGCCAA | G | T | Glu | End (1290) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa. | 2.20E-137 | |

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| 918 | cg43973762 | 165 | CAAGAAGCGA TTGAACACAAAT TA[G/C]CAGAGT ATCACAAATTGG CTAGAAA | G | C | Ala | Pro (1291) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa. | 2.20E-137 | |
| 919 | cg43973762 | 376 | GCCCTAAATAAA AAATGGGTTTG G[A/G]GGATACT TTAGAACAAATTG AATGCA | A | G | Glu | Gly (1292) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa. | 2.20E-137 | |
| 920 | cg42910848 | 443 | CCATGGTGCCA GGCCGTGCTCC CCA[G/C]GTGCC TCCGGGGTGCT GAAGATCTT | G | C | Pro | Arg (1293) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment). | 3.10E-132 | |
| 921 | cg29351416 | 537 | TTTCCCAAAAGT TCCAAAGTAGACA A[C/G]AGTAATC GCCTGTTACTG CAGCAGG | C | G | Asn | Lys (1294) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. | 3.20E-127 | |
| 922 | cg29351416 | 574 | GTTACTGCAGC AGGTCTCATTAC CA[G/T]ACATTC CTGGGAACTATA CCGTCAG | G | T | Asp | Tyr (1295) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa. | 3.20E-127 | |
| 923 | cg43938372 | 481 | TGTTTCCCACT TAATTTATTTTT [C/T]CTGCTTGTT CTTCTGTTTCA TCCT | C | T | Gly | Glu (1296) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD40376 PTD013 - HOMO SAPIENS (HUMAN), 243 aa. | 1.50E-123 | |

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| 924 | cg44930828 | 658 | CCTCAAGGTTTC GCTGCCGAAGC TT[G/A]CCAACG TGCAGCTCCTG GATACCGA | G | A | Ala | Thr (1297) | NON- CONSERVATIVE | UNCLASSIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 | |
| 925 | cg44930828 | 680 | CTTGCCAAACGT GCAGCTCCTGG ATA[C/T]CGACG GGGGTTTGTG CACTCGGAC | C | T | Thr | Ile (1298) | NON- CONSERVATIVE | UNCLASSIFIED | Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa. | 3.10E-122 | |
| 926 | cg44035718 | 919 | CTGGAGTACCA GGAAGAACTGA GGT[C/T]CCACT ACAAGGACATG CTCAGCGAA | C | T | Ser | Phe (1299) | NON- CONSERVATIVE | UNCLASSIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA83010 KIAA1058 PROTEIN - HOMO SAPIENS (HUMAN), 1534 aa (fragment). | 2.20E-121 | 2 |
| 927 | cg44921277 | 571 | TTGGCGCAACTT CCCCATCACCTT C[G/A]CCTGCTA TGCGGCCCTCT TCTGCCT | G | A | Ala | Thr (1300) | NON- CONSERVATIVE | UNCLASSIFIED | Human Gene Homologous to SWISSPROT-ACC:Q35682 MYELOID UPREGULATED PROTEIN - Mus musculus (Mouse), 296 aa. | 1.70E-120 | |
| 928 | cg43250166 | 461 | GCCGTGATTG CTCCAGTGCCA TCT[C/T]GTGCA GATGCTCATCTC GGCTCTCG | C | T | Glu | Lys (1301) | NON- CONSERVATIVE | UNCLASSIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43382 HYPOTHETICAL 146.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 1296 aa. | 3.30E-102 | 2 |

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| 929 | cg39512856 | 344 | CTTTTCCAGGC TTCAGCAACG AG[G/A]TTTCTTC CTTCGTTGCAAT TTCCAG | G | A | Thr | Ile (1302) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 930 | cg39512856 | 517 | GCCGTTCCACCTT CTGATATCCCC TTC/TCCGGCGA TAACCAGGTAA ATTTC | C | T | Gly | Glu (1303) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 931 | cg39512856 | 536 | TCCCTCCCCG CGATAACCCAGG TAA[A/C]ATTTTC CGGTAACGGAC CGAGTTCA | A | C | Phe | Val (1304) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 932 | cg39512856 | 638 | TGGTCTTCAACG AGATGCCACGA TG[C/A]CTCATC ACTGTTGAAAC AGCCACA | C | A | Ala | Ser (1305) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa. | 1.20E-98 | |
| 933 | cg39570960 | 851 | GCCTCCAGGAA GTCGTTTGTGTT TG[A/G]GCTGAA CGAATGTGCGT CCAGCCGC | A | G | Glu | Gly (1306) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O14997 3-7 GENE PRODUCT - HOMO SAPIENS (HUMAN), 709 aa (fragment). | 2.60E-93 | |
| 934 | cg43980391 | 510 | AGTAAATGGACA AGAATATCATCT T[C/T]AACTTGTA GACACAGCCGG GCAAGA | C | T | Gln | End (1307) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q15382 RAS-RELATED GTP- BINDING PROTEIN - HOMO SAPIENS (HUMAN), 184 aa. | 2.10E-90 | 1 |
| 935 | cg43983527 | 991 | TTCTGGAAGGAT GGTGCACCCCTG GT[G/T]CGGCCG CCATTACTGCCA GAGTCTG | G | T | Cys | Phe (1308) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa. | 6.50E-90 | 3 (11q23.3) |

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|-----|------------|------|---|---|---|-----|---------------|--------------------------|------------------|--|----------|----|
| 943 | cg43918287 | 676 | TAAACAGGCC AGCCGCCAAC CCC[A/G]AAAGT TGGCTGCAGTT ATATTAAT | A | G | Leu | Ser (1316) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment). | 7.30E-84 | |
| 944 | cg43918287 | 693 | CAACCCCAAA AGTTGGTCTGC AGTT[C]ATATTA ATTGAGGTTGG ACCTGGG | T | C | Ile | Met (1317) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment). | 7.30E-84 | |
| 945 | cg37027086 | 217 | GAATCAGAACTA CAAGGATCAATT A[T/C]CCCAGCT CAATGTCAGGG TTCTTCA | T | C | Ser | Pro (1318) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA76824 KIAA0980 PROTEIN - HOMO SAPIENS (HUMAN), 1406 aa (fragment). | 1.20E-83 | |
| 946 | cg42688841 | 430 | ATTATAACTGGG ATCCCAGTCAAC A[T/A]AAGGTAG AATTCATTAAAC CTCAAG | T | A | Met | Leu (1319) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 | |
| 947 | cg42688841 | 598 | CCGAGCCTAGT GCCAGCGCGGC GGC[A/C]AGACA GAGCTGTCAGA GCGGCGACC | A | C | Cys | Gly (1320) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa. | 1.90E-83 | |
| 948 | cg40332814 | 339 | ACTGCACAGGG ACCGAATCTCTG CC[T/C]CCCGCT CTGCAGCCAGG TGCTCCAA | T | C | Glu | Gly (1321) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA74864 KIAA0841 PROTEIN - HOMO SAPIENS (HUMAN), 641 aa (fragment). | 3.10E-83 | 19 |
| 949 | cg43920571 | 2059 | GCGTTTTTCTCT CACGTCCTGCT GA[G/A]ATTACT GAGGAATATTGT GCTGGC | G | A | Ser | Phe (1322) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P34624 HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III - Caenorhabditis elegans, 548 aa. | 3.50E-82 | 10 |

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|-----|------------|-----|--|---|---|-----|---------------|--------------------------|------------------|--|----------|----------|
| 950 | cg44024149 | 451 | GGAAGCCGCAC TCAGTTATGGCT TC[T/C]ACGGCT GCCACTGTGGC GTGGGTGG | T | C | Tyr | His (1323) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa. | 5.30E-79 | 1 (1p35) |
| 951 | cg43307245 | 156 | GATATGATAGCT TGTCCTGAAACT G[A/G]GACTCCT GCCGTGATAAC GTGTGAC | A | G | Glu | Gly (1324) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15488 GLYCOGENIN-2 ALPHA - HOMO SAPIENS (HUMAN), 501 aa. | 1.00E-75 | X |
| 952 | cg39523553 | 698 | GTGTGAGGTCT GCCCGATCCGG GAT[G/A]GCTGC CGGTGGGTGAT CGACGGTAG | G | A | Gly | Ser (1325) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 | |
| 953 | cg39523553 | 861 | ATGGCTCTTTCC GCCTGGCCCCGA GC[T/C]CGATCA GGCATCAAGGT GCCTGGAA | T | C | Leu | Pro (1326) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 | |
| 954 | cg35933325 | 312 | ACCAAATGCCA CTATTTTTTCTC CC[A/C]TTGCCA AAAATGAAGGAA ATCACGT | A | C | Asn | Lys (1327) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA74845 KIAA0822 PROTEIN - HOMO SAPIENS (HUMAN), 1581 aa. | 2.40E-74 | |
| 955 | cg41677120 | 325 | CACGACCCACG AGATCATGGGG CCC[A/G]AGAAA AAGCACCTGGA CTACTTAAT | A | G | Lys | Glu (1328) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 1.10E-71 | 11 |

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| 956 | cg41677120 | 330 | CCCACGAGATC ATGGGGCCCAA GAA/CJAAGCA CCTGGACTACTT AATTCAGT | A | C | Lys | Asn (1329) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 1.10E-71 | 11 |
| 957 | cg41677120 | 382 | CACAAATGAGAT GAATGTGAACAT C[C/T]CACAGTT GGCAGACAGTT TAATTTGA | C | T | Pro | Ser (1330) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa. | 1.10E-71 | 11 |
| 958 | cg39648832 | 208 | TGCAGCCTCGT CCTCCTCCTCTG GC[A/T]GGCTCT GCACACTCTGC TCCTGGTA | A | T | Leu | Gln (1331) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA76807 KIAA0963 PROTEIN - HOMO SAPIENS (HUMAN), 1366 aa. | 3.20E-70 | |
| 959 | cg42696021 | 412 | GACACCCGCAC CCGGGCATGCT TCA[C/G]ACAGT GGCTGTGCCGC CTTCACAAT | C | G | Thr | Arg (1332) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa. | 1.40E-69 | |
| 960 | cg42696021 | 421 | ACCCGGGCATG CTTCACACAGTG GC[T/C]GTGCCG CCTTCACAATGA AGTGAAC | T | C | Leu | Pro (1333) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa. | 1.40E-69 | |
| 961 | cg34243633 | 269 | CAGAGATAATG CAGGCCAGGGA GGA[G/C]ATTGC ACTGGATGTCA CCATCATGG | G | C | Ile | Met (1334) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa. | 1.30E-68 | |

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| 968 | cg44938009 | 1289 | GAGTGCACGCA TAAAGATGGAA GAG[G/T]ATGCA CTACTTTCTGAT CCAGTGGA | G | T | Asp | Tyr (1341) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:Q43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO- TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) - Homo sapiens (Human), 587 aa. | 5.80E-66 | X |
| 969 | cg43949821 | 287 | ATTTTAATTCCT TCCTGTCTACG GC[G/A]GTTGGA CCTCCTGGCTC TCTGCTGT | G | A | Arg | Cys (1342) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD34394 NUCLEAR PORE COMPLEX INTERACTING PROTEIN NPIP - HOMO SAPIENS (HUMAN), 350 aa. | 3.80E-62 | |
| 970 | cg39516123 | 681 | TGGCTTCGGCT GGCGGGCCATC AAT[C/T]CCAGC ATGGCTGCCCC CAGCAGTCC | C | T | Pro | Ser (1343) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 5.10E-62 | |
| 971 | cg42731307 | 347 | CGAAAAGCAAA GTGCAGTTTGT GC[T/C]TCGGCT GTTGAGTGGTT CGGTTCCA | T | C | Ser | Gly (1344) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.60E-61 | |
| 972 | cg42731307 | 488 | TCTGAAAGAA GGCATTGATGAT CC[G/A]GTCCCC CAGTGGGTTGA TGGCAAGT | G | A | Arg | Trp (1345) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.60E-61 | |
| 973 | cg42731307 | 524 | GGTTGATGGC AAGTTCTGGAAT CC[T/C]CTGGAA ATCTCCCCGGCT GAGAGTC | T | C | Arg | Gly (1346) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa. | 2.60E-61 | |
| 974 | cg44910937 | 648 | TGCCCTTTGGAAC AGGAATATGAAA A[G/T]AAACTCA GAGCCGAGTTA GTGGAAA | G | T | Lys | Asn (1347) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q20716 F53B7.3 - CAENORHABDITIS ELEGANS, 267 aa. | 2.60E-61 | 3 |

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| 975 | cg43335624 | 149 | TCGAAAGGAAG TGAGTGCAGAT GGG[A/G]AGACC ATCACTGTCACT TTCCTTAA | A | G | Lys | Glu (1348) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q62184 T-COMPLEX PROTEIN 10C (TCP-10) - MUS MUSCULUS (MOUSE), 438 aa. | 7.00E-61 | |
| 976 | cg43277268 | 448 | CGCTAATGCCA AGAAGGAGATG GTG[C/A]GCTCC AAGCTGCCCAA CAGTGTGCT | C | A | Arg | Ser (1349) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD45423 EH DOMAIN-CONTAINING PROTEIN EHD1 - MUS MUSCULUS (MOUSE), 534 aa. | 3.90E-60 | |
| 977 | cg44128084 | 724 | CTTGACATCCAG CCAGACGGTTC AG[A/G]ATCAGC GGTCTGTGGT | A | G | Glu | Gly (1350) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.70E-59 | |
| 978 | cg30455661 | 322 | TTCTCAAGTGGT TTGAAGTCAAC A[G/T]ATTTCAC AGAAGAAATCA GCCCTC | G | T | Gln | His (1351) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa. | 5.20E-58 | |
| 979 | cg42747615 | 31 | TGTGATAAAAGT CACTTTCAGGC CA[T/C]TCACAG CGAATCTTCAGA CACTTT | T | C | Ile | Thr (1352) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q14693 HYPOTHETICAL PROTEIN KIAA0188 - Homo sapiens (Human), 899 aa (fragment). | 1.80E-57 | |
| 980 | cg43153425 | 276 | ACAAATTACTAT GGGTTCTACTG AA[T/G]CTCGGG TTGACTACATGG GCTCAAG | T | G | Ser | Ala (1353) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment). | 2.40E-57 | |
| 981 | cg43968980 | 1093 | TATTTCTGCTT CTCTAACAGCTG A[C/A]TGTGAATT GCTTCCTTGA CTGAAG | C | A | Ser | Ile (1354) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa. | 2.50E-56 | 5 |

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| 982 | cg30384142 | 173 | GATAGTGGTGT GTGGTGATGCG AGTATTAACCT GACGAATGGTT AGCTGAAAT | A | T | Lys | End (1355) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P44788 SUN PROTEIN (FMU PROTEIN) - Haemophilus influenzae, 451 aa. | 5.30E-56 | |
| 983 | cg43957773 | 445 | GGGCTCACCGT AGAGCAACTGC AATC[A]GCTCT GGCCTGGGCC TGGACAGGA | C | A | Asp | Tyr (1356) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O43914 DNAX ACTIVATION PROTEIN 12 - HOMO SAPIENS (HUMAN), 113 aa. | 3.30E-54 | 19 |
| 984 | cg43931038 | 464 | AGGGCAACTTG TGGCAACCTG GTC[A/C]AGGAA ACCTTGACTTCT TCAAAATTC | A | C | Leu | Trp (1357) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 985 | cg43931038 | 588 | CCTCCCCCAT GCGATGCCCAA CAC[T/C]TTTGC GAGTGATGGGC TTGAAAGGG | T | C | Ser | Gly (1358) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa. | 6.10E-54 | 11 |
| 986 | cg43971060 | 686 | CCCACCTCGTT CGTGCTCCAC CCT[C/T]CCCAG CTCCACCGCCT GGTCTTCAG | C | T | Pro | Ser (1359) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:P31639 SODIUM/GLUCOSE COTRANSPORTER 2 (NA+)/GLUCOSE COTRANSPORTER 2 (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 672 aa. | 4.20E-53 | |
| 987 | cg44010070 | 541 | TTCTCTGCCGG CACCTACCCGC GCC[T/G]GGAGG AGTACCGCCGG GGCATCTTA | T | G | Leu | Arg (1360) | NON- CONSERVATI VE | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O35775 SYNCOLLIN (SIP9) - Rattus norvegicus (Rat), 145 aa. | 6.40E-51 | |

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| 988 | cg43298242 | 145 | TCTGTTGGCAG GGCTCACAGAG ACG[G/A]GGGTG AGGGAGAGAT CGTGGGTTT | G | A | Pro | Leu (1361) | NON- CONSERVATIVE | water_ch annel | Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa. | 1.30E-163 | |
| 989 | cg43298242 | 163 | AGAGACGGGGG TGAGGGGAGAG ATC[G/A]TGGGT TCATGAGATCCC ATCTTGGG | G | A | Thr | Met (1362) | NON- CONSERVATIVE | water_ch annel | Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa. | 1.30E-163 | |
| 990 | cg43300636 | 440 | CCACAGCCGCC ACGCCACCTC CCG[G/gap]CCC AGGCCAGGCC TATGCGCATCA | G | gap | Gly | Gly (1363) | FRAMESHIFT | ATPase_ associat ed | Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATP SYNTHASE) (H(+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa. | 1.70E-175 | |
| 991 | cg43300636 | 446 | CCGCCACGCC ACCTCCCGGCC CAG[G/gap]CCCA GGCCTATGCGC ATCACCATGG | G | gap | Gly | Gly (1364) | FRAMESHIFT | ATPase_ associat ed | Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATP SYNTHASE) (H(+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa. | 1.70E-175 | |
| 992 | cg43250373 | 193 | CTGTGGGGTTG ACCCAGAACAA AGC[A/gap]TTGC CAGAAACGTTA AGTATGGGA | A | gap | Leu | Cys (1365) | FRAMESHIFT | ATPase_ associat ed | Human Gene Similar to TREMBLNEW-ID:G2921585 ECTO- ATPASE - MUS MUSCULUS (MOUSE), 495 aa. | 1.40E-100 | 10 (10q24) |

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| 999 | cg43303165 | 2549 | GGCCCCCACTA TCAGGGGCCCT GGC[C/gap]TCAA TCACTGAGACC ATCCAAGTCC | C | gap | Ser | Gln (1372) | FRAMESHIFT | histone | Human Gene Similar to SWISSPROT- ID:P53973 HISTONE DEACETYLASE HDA1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 706 aa. | 4.10E-70 | X |
| 1000 | cg42489148 | 881 | TGCGAGTGGAT GCGGAACCGGC GCA[G/gap]CAGT CCCTCGGCAGC CAAGTGAAAA | G | gap | Ser | Thr (1373) | FRAMESHIFT | homeobox | Human Gene Homologous to SPTREMBL-ID:O00503 CAUDAL- TYPE HOMEBOX PROTEIN 2 - HOMO SAPIENS (HUMAN), 313 aa. | 6.00E-118 | 13 |
| 1001 | cg43929210 | 483 | TCTGGCTCAGC ATGATGTTCCCT CT[G/gap]GCCTT CAGCCTGCCAC TAAAGAATG | G | gap | Ala | Ala (1374) | FRAMESHIFT | hydroxysteroid | Human Gene SWISSPROT- ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17-BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa. | 0.00E+00 | 5 |
| 1002 | cg44004587 | 1811 | GCTTATTTTCGG TGTTGAATAAGA A[G/gap]ACACTA AAAGCTCGATG CAATAATC | G | gap | Val | Val (1375) | FRAMESHIFT | isomerase | Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa. | 3.00E-123 | |
| 1003 | cg41501665 | 156 | CGCTTCTCCAA GGTGCTGGAGG AGG[C/gap]GGC GGCCGCCGAGG AGGGCCTGCC | C | gap | Ala | Gly (1376) | FRAMESHIFT | kinase | Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.70E-76 | |
| 1004 | cg41501665 | 184 | CGGCCGCCGAG GAGGGCCTGCG CGA[G/gap]CTGC AGCGCAGCCGG CGGCTCTGCC | G | gap | Leu | Cys (1377) | FRAMESHIFT | kinase | Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.70E-76 | |

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|------|------------|------|---|---|-----|-----|---------------|------------|--------------------|--|-----------|---------------|
| 1005 | cg41501665 | 202 | TGCGGAGCTG CAGCGCAGCCG GCG[G/gap]CTCT GCCACGAGGAC GTGGAGGCCG | G | gap | Leu | Ser (1378) | FRAMESHIFT | kinase | Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.70E-76 | |
| 1006 | cg41501665 | 232 | GCCACGAGGAC GTGGAGGCCGCT GGC[C/gap]GCC ATCTACGAGGA GAAGGAGGCCCT | C | gap | Ala | Pro (1379) | FRAMESHIFT | kinase | Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa. | 2.70E-76 | |
| 1007 | cg43939695 | 342 | CAAGACTGAGA TCAATTGCCCG CGG[C/gap]CGG ACGATGGGAAC CTCTTCCCCCT | C | gap | Pro | Arg (1380) | FRAMESHIFT | kinasere ceptor | Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15 (15q25) |
| 1008 | cg29023997 | 199 | TCTGGATGGGA TGGAGCACCAT GTG[C/gap]GCAC CTGCATCCCCA AAGTGGAGCT | C | gap | Arg | Ala (1381) | FRAMESHIFT | kinasere ceptor | Human Gene SWISSPROT- ID:P36896 SERINE/THREONINE- PROTEIN KINASE RECEPTOR R2 PRECURSOR (EC 2.7.1.37) (SKR2) PRECURSOR (EC 2.7.1.37) (SKR2) (ACTIVIN RECEPTOR-LIKE KINASE 4) (ALK-4) (ACTR-IB) - HOMO SAPIENS (HUMAN), 505 aa. | 9.30E-280 | 12 |
| 1009 | cg43983535 | 4377 | CTCCAACACAGCT TCTTCACCTTTT T[C/gap]AGAAGG GCTTCTGCAGC TACCAACT | C | gap | Leu | Leu (1382) | FRAMESHIFT | laminin | Human Gene SWISSPROT- ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa. | 0.00E+00 | 6 (6q22) |
| 1010 | cg42488873 | 480 | TTCCCCCTTAAAT TGGTCAGCATA GT[G/gap]CCCCA TTTTGGGGCATC CTTCAGCT | G | gap | His | Thr (1383) | FRAMESHIFT | lipase | Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa. | 9.80E-261 | |

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| 1011 | cg42488873 | 494 | GTCAGCATAGT GCCCCATTTTG GGG[C/gap]ATCC TTCAGCTGGAC AAGGGAACA | C | gap | Cys | Ser (1384) | FRAMESHIFT | lipase | Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa. | 9.80E-261 | |
| 1012 | cg42488873 | 923 | CACGCGGCCCC CCAGCCTCCTG CCC[G/gap]CCTC CGCGGCCGTGT GCGCGCCCGAG | G | gap | Ala | Gly (1385) | FRAMESHIFT | lipase | Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa. | 9.80E-261 | |
| 1013 | cg43249083 | 2329 | GGAGCAGCTCC AGGAGACGCTG CTG[C/gap]GGG CTCTTCGGGCT CTGGTGCTGAA | C | gap | Arg | Gly (1386) | FRAMESHIFT | nucl_rec pt | Human Gene SWISSPROT- ID:P20393 V-ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa. | 0.00E+00 | 17 (17q11.2) |
| 1014 | cg43991048 | 6644 | TCTTTCTTTTCTT CTTCTTTTTTTT C/gap]TGTTTTT CTGCTTTATCCT CTTCT | C | gap | Glu | Lys (1387) | FRAMESHIFT | nucl_rec pt | Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa. | 0.00E+00 | 17 |
| 1015 | cg43919677 | 4055 | GAAGAAAAGAA AGAATGCTACTA TA[A/gap]TCTCA ATGACGCCAGT CTCTGTGAT | A | gap | Asn | Ile (1388) | FRAMESHIFT | oncogene | Human Gene SWISSPROT- ID:Q00918 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1- BP- 1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT) - RATTUS NORVEGICUS (RAT), 1712 aa. | 0 | 2 (2p12) |

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| 1028 | cg39517655 | 438 | GGGGCCCTTAC TCGCTATGCTG CAA[G/gap]GGC CCCGGGCCTTG GCTTCGGCCGC | G | gap | Gly (1401) | FRAMESHIFT | transcript factor | Human Gene SWISSPROT- ID:Q14209 TRANSCRIPTION FACTOR E2F2 (E2F-2) - HOMO SAPIENS (HUMAN), 437 aa. | 1.4E-237 | 1 |
| 1029 | cg43954704 | 1391 | CCCACTGGAAG TGGAGGCTCCA GTC[A/gap]AACC CCCCCTTGAGC TCCGAGGCAG | A | gap | Phe (1402) | FRAMESHIFT | transferase | Human Gene Similar to SPTREMBL- ID:Q29121 UDP- GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa. | 1.1E-68 | 2 |
| 1030 | cg43986426 | 1227 | GCGGACAGTCG CCCTAAGCAGT GCA[A/gap]GGTG TCTTGAGCCCTA TGGTGGCCA | A | gap | Gly (1403) | FRAMESHIFT | ubiquitin | Human Gene SWISSPROT- ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa. | 0 | 1 |
| 1031 | cg43917221 | 2853 | GAAATGTCATCC ACGGTATTTTT TT[gap]CAGTTT TAGTTTGACCAA AGCTTTA | T | gap | Lys (1404) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q13563 POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYSTWIN) (R48321) - Homo sapiens (Human), 968 aa. | 0 4 (4q21) | |
| 1032 | cg43918356 | 2640 | ATGTCATCTTCA TCTAGAAACGC CC[gap/A]TCACG GAAATGGAATTG CTGCCAGA | gap | A | Met (1405) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment). | 0 | 12 |
| 1033 | cg43918446 | 2812 | CTTTCCACATG ACTTGTTACATT C[C/gap]GACCAC TGGGACCACTC GGTGAGCT | C | gap | Ser (1406) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa. | 0 | |

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| 1034 | cg43927750 | 2857 | TAAAGTTATTC TCCAATGGTGAT T[G/gap]GGCAAG CCCTGCCTCCT GTATTCTT | G | gap | Pro | Pro (1407) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:Q13496 MYOTUBULARIN - Homo sapiens (Human), 603 aa. | 0 | X (Xq28) |
| 1035 | cg43961075 | 1344 | GGGTAGGATTG CTCATTTTCAGGG CA[G/gap]CTGTC GCAAGCATCTC CCACCCCGT | G | gap | Ser | Ser (1408) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P49746 THROMBOSPONDIN 3 PRECURSOR - Homo sapiens (Human), 956 aa. | 0 | 1 |
| 1036 | cg43961763 | 1192 | CATCTAGGTCAA CAGGAAGGTCA AG[C/gap]TCCCG CTCCGGTTCCA CTGATCCAT | C | gap | Glu | Asp (1409) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P13521 SECRETOGNANIN II PRECURSOR (SGII) (CHROMOGRANIN C) - Homo sapiens (Human), 617 aa. | 0 | 2 |
| 1037 | cg43968223 | 2979 | GTTCTGTTCTTG TAGCGCTTTCTG C[G/gap]CTGCAG CATGATCTGAAG CTTGTTG | G | gap | Arg | Ala (1410) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment). | 0 | 14 |
| 1038 | cg43980727 | 2673 | CCCTCCAGGTA GAGGCCTAGGA AGG[C/gap]CCCA GAACTGAAGCC GAAGCGCTGG | C | gap | Ala | Pro (1411) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa. | 0 | 17 |
| 1039 | cg43999667 | 3941 | TTCTGTTTTGTC AGGACTTTTTTT TT[G/gap]CTACAA GTTGTTTTTCTG GGATCAC | T | gap | Glu | Glu (1412) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment). | 0 | 6 |
| 1040 | cg44022781 | 3927 | GTATCAAAAGTGC TCTTTCCAACCT TT[G/gap]GGAGGC CCCATCACCACT ACCGGTA | T | gap | Pro | Pro (1413) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q14692 KIAA0187 PROTEIN - HOMO SAPIENS (HUMAN), 1282 aa. | 0 | |

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| 1041 | cg44919370 | 571 | CGTGGACTTTTC CGAGGATGACC CC[C/gap]TGGAG GCCACTGTCCA TTGGGCCCC | C | gap | Leu | Trp (1414) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60624 CLASS I CYTOKINE RECEPTOR - HOMO SAPIENS (HUMAN), 636 aa. | 0 | 19 |
| 1042 | cg44932924 | 2612 | TCTACAACCAGA GCCAGGAATTA CA[G/gap]ACGAA GCTGGAGGACT GCAGGAACA | G | gap | Thr | Arg (1415) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q92574 HAMARTIN (MYELOBLAST KIAA0243) - HOMO SAPIENS (HUMAN), 1164 aa. | 0 | 9 |
| 1043 | cg43991434 | 1167 | GGGTGCAAGG GCCTTGGGGAA ATA[G/gap]TCCT GCTGCACCATG TGGTTCAGCG | G | gap | Asp | Asp (1416) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SWISSNEW- ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa. | 1.7E-304 | 22 |
| 1044 | cg44931278 | 1264 | CCTCCTCCAGG GAAGCACTGGC CAG[G/gap]TCCT GCAGTGTAGGC CACTTCTGCA | G | gap | Asp | Asp (1417) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q15830 MUTY HOMOLOG - HOMO SAPIENS (HUMAN), 535 aa. | 4.5E-280 | 1 |
| 1045 | cg43949042 | 427 | CACAGCTGCGT TGCCATAGTTGC CC[T/gap]GGAAA AAGCGGCCCCAC GAACCAGGC | T | gap | Gln | Arg (1418) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O75907 ACAT RELATED GENE PRODUCT 1 - HOMO SAPIENS (HUMAN), 488 aa. | 6.10E-268 | |
| 1046 | cg43972066 | 2313 | TAAATTGACTT TTCTCATGTAAA A[A/gap]TGTCTA ATGCGATGTATT TGGTAAT | A | gap | His | His (1419) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O60747 PUTATIVE G-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 562 aa (fragment). | 4.10E-221 | 10 |

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| 1047 | cg43955639 | 723 | GGGGGACTGG GGACCTCGTCT GTT[G/gap]GGTT CCCCTCCTCCA GGGTAGCGGC | G | gap | Pro | Gln (1420) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment). | 2.80E-215 | |
| 1048 | cg43955639 | 725 | GGGTACTGGGG ACCTCGTCTGTT GG[G/gap]TTCCC CTCCTCCAGGG TAGCGGCTC | G | gap | Asn | Asn (1421) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment). | 2.80E-215 | |
| 1049 | cg43965656 | 391 | CTGCCTATTCTG AACCAGCCAAC AT[C/gap]TGAGA TTGTTGCCAATG CCCCGAGGT | C | gap | Ser | Leu (1422) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:Q99541 ADIPOPHILIN - HOMO SAPIENS (HUMAN), 437 aa (fragment). | 7.20E-210 | |
| 1050 | cg43944615 | 2370 | TACATGGCACA GAGGAAGAAGC GCA[G/gap]CAC GGCGCTGCAGT TCACGTCCACC | G | gap | Leu | Cys (1423) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SPTREMBL- ACC:O14877 FRPHE - HOMO SAPIENS (HUMAN), 346 aa. | 1.30E-192 | |
| 1051 | cg43323906 | 334 | CTCTGGTGCTG CTCCTCTGAAGA TT[C/gap]AAGCT TATTTCAATGAG ACTGCAGA | C | gap | Gln | Lys (1424) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P42081 T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2 ANTIGEN) (CTLA-4 COUNTER- RECEPTOR B7.2) (B70) (FUN-1) (BU63) - Homo sapiens (Human), 329 aa. | 1.80E-174 | |
| 1052 | cg44004690 | 251 | GAGGAGGAGGA GGTGGAGGAGG AGG[A/gap]GGG AGAAAGAGGATG TTTTACCCGAG | A | gap | Glu | Gly (1425) | FRAMESHIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAAT4892 KIAA0869 PROTEIN - HOMO SAPIENS (HUMAN), 888 aa (fragment). | 2.50E-161 | |

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| 1053 | cg44004690 | 402 | ACCGGAGAGTG GGCACCCCGTC CCA[G/gap]GGG CCATTTCTTCGA GGGAGCACCA | G | gap | Gly | Gly (1426) | FRAMESHIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA74892 KIAA0869 PROTEIN - HOMO SAPIENS (HUMAN), 888 aa (fragment). | 2.50E-161 | |
| 1054 | cg43957283 | 322 | TCGAGGGTGAC CACAGCCCCAG AGG[G/gap]CCG CAGCACAGCGC AGGGGGTGGCG | G | gap | Pro | Pro (1427) | FRAMESHIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD27734 CGI-25 PROTEIN - HOMO SAPIENS (HUMAN), 301 aa. | 1.40E-160 | |
| 1055 | cg43329741 | 336 | GCTCTACCTGG GCTACACCCCG CAG[G/gap]CGG CCCGTGAAGTG CGCATCATGCA | G | gap | Ala | Arg (1428) | FRAMESHIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD39906 FH1/FH2 DOMAIN- CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa. | 6.70E-159 | |
| 1056 | cg44010310 | 501 | TTTGTGAGATG CATGAAATTTTT T[gap /T]CTCTATT GCTGCTTGAAAA TTTACA | gap | T | Lys | Lys (1429) | FRAMESHIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:BAA32101 BCAP - HOMO SAPIENS (HUMAN), 331 aa. | 1.30E-155 | 13 |
| 1057 | cg39729127 | 981 | GCTCTCTCTTT ATTGGTAACCAG T[gap /T]GGTGGC CACGAGTCATA CAGGGAAA | gap | T | Val | Val (1430) | FRAMESHIFT | UNCLAS SIFIED | Human Gene TREMBLNEW- ACC:AAD42876 NY-REN-45 ANTIGEN - HOMO SAPIENS (HUMAN), 815 aa. | 3.00E-152 | 1 |
| 1058 | cg43135797 | 861 | AGATCTGTCTCC CCGGAGACCCCG GA[G/gap]CCGCT GGCCATTGCAG AAGGCGCCC | G | gap | Leu | Ser (1431) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O14732 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE 2 (EC 3.1.3.25) (IMP 2) (INOSITOL MONOPHOSPHATASE 2) (MYO- INOSITOL MONOPHOSPHATASE A2) - Homo sapiens (Human), 288 aa. | 1.60E-150 | 18 |

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| 1059 | cg43965796 | 1704 | ATCACTGTTGAT GCTCTGGGCCA CG[C/gap]CAGG GTACTGGATCTT CATGGCCAC | C | gap | Gly | Ala (1432) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment). | 9.00E-148 | 1 |
| 1060 | cg43965796 | 1705 | TCACTGTTGATG CTCTGGGCCAC GC[C/gap]AGGG TACTGGATCTTC ATGGCCACC | C | gap | Gly | Ala (1433) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment). | 9.00E-148 | 1 |
| 1061 | cg42907867 | 1100 | AGGGCCACGGG GTGGGCCAGGG GGC[C/gap]GGG CCATTCCAGTG GCTCCTTGTC | C | gap | Arg | Arg (1434) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q99769 HYPOTHETICAL 26.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 255 aa. | 1.10E-140 | 1 |
| 1062 | cg43922710 | 126 | TCTACCCAGCTA AATACACATTAT G[G/gap]CATTTA GCAAACTAACTT ACAAGTC | G | gap | Ala | His (1435) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:BAA74897 KIAA0874 PROTEIN - HOMO SAPIENS (HUMAN), 601 aa (fragment). | 4.90E-140 | |
| 1063 | cg43303845 | 1073 | GCAGGAACGCC TGGATCGGGAG AGG[C/gap]AAGA AAGACAAGAAC GAGAGAGGCT | C | gap | Gln | Lys (1436) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa. | 1.90E-138 | |
| 1064 | cg43973762 | 430 | ATAACAGAAAAGC AAGAGAAAGTG GA[G/gap]AACTC TGAAAGAAAGAA GTTCAAAAAG | G | gap | Arg | Lys (1437) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa. | 2.20E-137 | |

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| 1065 | cg43918679 | 411 | TCACAGATATCT CCATTGCCAG GA[G/gap]ATGCC CAGCCTGGAGG TGATCACGC | G | gap | Met | Cys (1438) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa. | 3.00E-131 | 21 |
| 1066 | cg38059286 | 503 | GCCGCTCCCTC TTCTCACTGAAG CA[G/gap]ATCTT CCAGGAGGACA AAGACCTGG | G | gap | Ile | Ser (1439) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD39906 FH1/FH2 DOMAIN-CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa. | 4.00E-129 | |
| 1067 | cg42549778 | 1014 | ACTGTCACCTCC CTGCTGCAGGG CA[G/gap]CCCCC ACCTGTGAGTG GCTCGAGCC | G | gap | Ser | Thr (1440) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD29690 PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1 - MUS MUSCULUS (MOUSE), 267 aa. | 3.70E-126 | |
| 1068 | cg44921277 | 516 | CCCTGATCATCC TCATCGTGGAG CT[G/gap]TGCGG GCTCCAGGCC GCTTCCCCC | G | gap | Cys | Ala (1441) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O35682 MYELOID UPREGULATED PROTEIN - Mus musculus (Mouse), 296 aa. | 1.70E-120 | |
| 1069 | cg44921277 | 518 | CTGATCATCCTC ATCGTGGAGCT GT[G/gap]CGGG CTCCAGGCCCG CTTCCCCCTG | G | gap | Cys | Ser (1442) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SWISSPROT-ACC:O35682 MYELOID UPREGULATED PROTEIN - Mus musculus (Mouse), 296 aa. | 1.70E-120 | |
| 1070 | cg42530218 | 327 | GATTTAATACAC AGCAGCAGCAG CA[gap/G]AACTA CATTAGGTGGT CTCTTCAGT | gap | G | Gln | Gln (1443) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa. | 2.00E-118 | |

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| 1071 | cg42530218 | 329 | ATTAAATACACA GCAGCAGCAGC AA[A]gap]CTACA TTAGGTGGTCTC TTCAGTCA | A | gap | Thr | Leu (1444) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa. | 2.00E-118 | |
| 1072 | cg43325007 | 979 | AGGATACCCCC GAGGAAGGCCG CCA[G]gap]GAAT GCGTGTGCTGG GTAGGTCTTG | G | gap | Leu | Trp (1445) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa. | 4.80E-110 | 20 |
| 1073 | cg43981269 | 776 | GGCCTACGGCG CCTACGCTCAG GCA[C]gap]TGAT GCAGCAGCAAG CGGCCCTGAT | C | gap | Leu | End (1446) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to SPTREMBL-ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa. | 4.50E-105 | |
| 1074 | cg43250166 | 166 | AGGTGGCCCTC ACACCCAGTGC TGT[G]gap]CTGC GCGGAGGGCTG TACTGAAGGT | G | gap | Ala | Asp (1447) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Homologous to TREMBLNEW-ACC:CAB43382 HYPOTHETICAL 146.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 1296 aa. | 3.30E-102 | 2 |
| 1075 | cg43982164 | 778 | CTGCGGCGGGT GCTCATCCTGG ACA[gap]C]ATTTC ACCTGCCTCCTA TGCTCTTCCA | gap | C | Asn | Thr (1448) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O15194 HYA22 - HOMO SAPIENS (HUMAN), 340 aa. | 1.00E-90 | |
| 1076 | cg43980889 | 812 | TTAAATATAGAC AAGTGGACCAT TTT[gap]GCCCTCA AATTCACAGGA GCCAGCAT | T | gap | Ala | Pro (1449) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa. | 4.50E-89 | |

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| 1077 | cg43970119 | 832 | GTGGCCATTGG TGAGACATCCAT CA[A/gap]TATTG CAAACCAAAAGT TTTATTTTC | A | gap | Ile | Met (1450) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:O88719 CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLTRANSFERASE) (CMP- SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE) - MUS MUSCULUS (MOUSE), 432 aa. | 1.00E-82 | 12 |
| 1078 | cg44030987 | 447 | TCGGCATGTTG AGTGGAACAGT TGT[A/gap]TTTA CTTGAATTCCTCA TCTCCTTCT | A | gap | Tyr | Thr (1451) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA76495 TYPE II MEMBRANE PROTEIN SIMILAR TO CD69 - HOMO SAPIENS (HUMAN), 149 aa. | 1.90E-81 | |
| 1079 | cg43320682 | 665 | GGTGGCTCAGG GGCTGGGGGAG GCT[C/gap]CCCT GGGGCTTCAGA CAGCACATAG | C | gap | Glu | Ser (1452) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment). | 6.60E-81 | |
| 1080 | cg25255686 | 366 | AAGGCACCATC AAGTCGGCGGT GGC[C/gap]TTCG GGCATCTCCTT GCCGAGGGTA | C | gap | Phe | Ser (1453) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB39700 CONSERVED HYPOTHETICAL PROTEIN - STREPTOMYCES COELICOLOR, 384 aa. | 2.10E-77 | |
| 1081 | cg43988975 | 371 | CTCCTCCTGAC CGAGTGGGCCG GCA[G/gap]GAG CTTGAAATCGTC ATTGGAGATG | G | gap | Glu | Ser (1454) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:P50606 MAGO NASHI PROTEIN HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 146 aa. | 8.00E-76 | |
| 1082 | cg39523553 | 670 | CACTGGTATGC ACGGCGCGGTC TCC[G/gap]CAGT GTGAGGTCTGC CCGATCCGGG | G | gap | Gln | Ser (1455) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa. | 7.20E-75 | |

| | | | | | | | | | | | | |
|------|------------|------|---|-----|-----|---------------|---------------|------------|------------------|--|----------|----|
| 1083 | cg43951096 | 2953 | CTCCCTCCTGG GTATCTGCATCT TC[gap]/AJAAAAAT CTCCTTCTTGGT TTTCATCC | gap | A | Glu | End (1456) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa. | 2.00E-71 | 17 |
| 1084 | cg42831353 | 806 | GGACACAGGCT GCGGTGTAAGC CCG[C/gap]GTCA CCGCCGGCACC TGCAGGAACT | C | gap | Thr (1457) | Thr (1457) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa. | 1.30E-67 | 22 |
| 1085 | cg44938009 | 688 | AATACTCCGTGC AGCGAGTGCGT CA[G/gap]CTCCG TGAAGAATTGTA TCAAGGTC | G | gap | Leu | Ser (1458) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SWISSNEW- ACC:O43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO- TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) - Homo sapiens (Human), 587 aa. | 5.80E-66 | X |
| 1086 | cg43054992 | 315 | CAAAATCACAGC TGAAGAAATGTA T[G/gap]ATATAT TTGGGAAATATG GACCTAT | G | gap | Asp | Ile (1459) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:AAD34105 CGI- 110 PROTEIN - HOMO SAPIENS (HUMAN), 125 aa. | 4.60E-64 | 2 |
| 1087 | cg39516123 | 928 | CCTGGGGCTCA CCAAGGCAACC TGG[C/gap]CTCC GGTCTTCATAGC AATGCAATA | C | gap | Ala | Ala (1460) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa. | 5.10E-62 | |
| 1088 | cg43983590 | 713 | GGAGGAGCCAG GCGAGCACACC CCC[C/gap]TGT GGCCCCTGCCA CGGCCAGCC | C | gap | Leu | Cys (1461) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SPTREMBL- ACC:Q19498 SIMILAR TO MELIBIOSE CARRIER PROTEIN - CAENORHABDITIS ELEGANS, 501 aa. | 1.50E-60 | |

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| 1089 | cg44128084 | 499 | CGCGGGCGCAT GCTCGACGTTT TGG[C/gap]GTCT GTCGACGAGTT GCCGGTGCAA | C | gap | Ala | Gly (1462) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SP TREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.70E-59 | |
| 1090 | cg44128084 | 524 | CGTCTGTCGAC GAGTTGCCGGT GCA[A/gap]CGCT GGAGCTGCGAC GGGATCCTGG | A | gap | Arg | Ala (1463) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SP TREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa. | 1.70E-59 | |
| 1091 | cg43976473 | 931 | GGCCCTGTGCT TGGAGCCGTGG GCT[C/gap]CGTA GCCCGAGTGAT AAGCCATGGC | C | gap | Gly | Glu (1464) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SP TREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa. | 3.50E-59 | 11 |
| 1092 | cg40309770 | 385 | TTCCGGCCGCC GCGTCCAGGGC TCG[C/gap]CCGC TGAGGTCGTTT ATGACCCCGC | C | gap | Gly | Gly (1465) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to SWISSPROT- ACC:Q60870 POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106) - Mus musculus (Mouse), 185 aa. | 4.10E-56 | |
| 1093 | cg42725664 | 184 | AGATAGCTGAG AATATTCTGCGC AA[G/gap]CCCTCA CAGCTTGTTTCC TGCGAGCC | G | gap | Leu | Leu (1466) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:BAA74896 KIAA0873 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa (fragment). | 1.5E-51 | |
| 1094 | cg39380052 | 497 | ATGAGATCGAC GCCTTGCGCGG CCG[C/gap]GGC GTAGACATTCC GCACCCGCTCA | C | gap | Gly | Ala (1467) | FRAMESHIFT | UNCLAS SIFIED | Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa. | 1.3E-50 | |

| | | | | | | | | | | | | |
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| 1095 | cg44928804 | 1181 | CTCTCAATCATG CCGCTTTAGAG AA[T/gap]GCAAC ATGGGCAACCT GATTGTGA | T | gap | Cys | Ala (1468) | FRAMESHIFT | UNCLAS SIFIED | Human Gene SWISSPROT- ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO- NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa. | 9.1e-313 | 6 (6q14) |
|------|------------|------|--|---|-----|-----|---------------|------------|------------------|--|----------|----------|

[illegible]

- ☒ I hereby claim the benefit under Title 35, United States Code, § 119(e) or §120 of any United States application(s), or §365(c) of any PCT International application(s) designating the United States of America listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

| Application No. <i>(U.S.S.N.)</i> | Filing Date <i>(dd/mm/yy)</i> | Status <i>(Patented, Pending, Abandoned)</i> |
|---|---|--|
| 60/167,383 | November 24, 1999 | Pending |

PCT International Applications designative the United States:

| PCT Appln No. | US Serial No. | PCT Filing Date | Status |
|----------------------|----------------------|------------------------|---------------|
| | | | |

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or patent issued thereon.

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TRADOCS:1403394.1(%2V601!.DOC)

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<221> misc_feature
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51

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CG43074195

<223> Accession number cg43074195

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51

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<222> (0)...(0)

<223> Accession number cg43988092

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50

<210> 42

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<223> Accession number cg43953517

<400> 42

aagttottgt agtaggtagg gggattact agggatatct gtggcatgat t

51

<210> 43

<211> 51

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<213> Homo sapiens

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<222> (26)...(0)

<223> single nucleotide polymorphism

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43953517

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<223> Accession number cg43953517

<400> 46

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<210> 47

<211> 50

<212> DNA

<213> Homo sapiens

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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43953517

<400> 47

attaatttgg ggttcattt gcttcttttc tttatgctta gattatctta

50

<210> 48

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<212> DNA

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<210> 49

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<223> Accession number cg43294632

CG43953517

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<210> 53
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<212> DNA
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51

<210> 54
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51

<210> 55
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51

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tacagacata agtgagcctc actgggaatt ttttcaacag tagtccagat c

51

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51

<210> 58
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<400> 58
ccagatcttg agatcttcag aaatgtagga atcaatgctt atttgtgtga g

51

<210> 59
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51

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51

<210> 61
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51

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51

<210> 65
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<400> 65

agggcagccc ctcagaagcc ttcccagcag atccggggac cccgttctgg t

51

<210> 66

<211> 51

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<223> Accession number cg43119489

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<211> 51

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<223> Accession number cg43957170

<400> 67

ctactaaaaa tacaaaaaat tagccaggcg tgggtggcgca tgcctgtagt c

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<211> 51

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<213> Homo sapiens

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<223> Accession number cg43957170

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51

<210> 69

<211> 51

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CGTCTTCTGG

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51

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50

<210> 71
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51

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aaagtctctg aaatgcttca tccccaacaa agcaaatttc atgtccgtca g

51

<210> 74
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<400> 74
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51

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51

<210> 76

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51

<210> 77

<211> 51

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51

<210> 78

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CG43948037

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<210> 79
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<210> 80
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<400> 82
cgctgcccgc gcggggacca caacccaagt cgcggccgcc gcagccatgc g

51

<210> 83
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51

<210> 84
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<223> Accession number cg43925424

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51

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<400> 85
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51

<210> 86
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<223> Accession number cg27803682

<400> 86
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51

<210> 87
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<223> Accession number cg43971768

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51

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<223> single nucleotide polymorphism

<221> misc_feature

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<222> (0)...(0)
<223> Accession number cg43987181

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aagcttagta ctaaaaagtc aaaatatttt tgcattgatag aggagtgtaa a

51

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51

<210> 90
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51

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51

CG43987181

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51

<210> 94
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51

<210> 95
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50

<210> 96
<211> 50
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51

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51

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tttgggatcc tgatcaattc tttctaattg tgttgaaaat gacaaagttg g

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tagaattttc tatccccccc cattttttcca gtaataaaaa gtagtgctgg g

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<210> 179

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51

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51

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CGCGCGCCAG CTATCGTCAG TGCCTGTTAT TGCCATTGGG TTTGTGACTG T

09710334 13250

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taaacatcta cagagttgaa acatactctg tcatattaataa tatattatct a

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50

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CG43258867
CG42907867
CG43920176

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<400> 230
aaagctgctt tgtaggttc cttatTTTTT attactgtc tttctcagt t 51

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51

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51

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51

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50

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<223> Accession number cg43963595

<400> 246
atgttacagt atgtacaaga cccctccctc gggggacggg goggactccg

50

<210> 247
<211> 51
<212> DNA
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<220>
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<223> single nucleotide polymorphism

<221> misc_feature
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<223> Accession number cg43992566

<400> 247
aaatagagaa tccagaccct tcccaaataa tttaagaact gagttttcct c

51

<210> 248
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43992566

<400> 248
atttaaattct gaagcagaaa aaaaagacaa ttacaaaga attattgagc

50

<210> 249
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
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<221> misc_feature
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<400> 249
tccctgcacg cctttacgtc agactatcac cacaagagcc ttgagtgtcc a

51

<210> 250
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<223> Accession number cg42697161

<400> 250
acgtggtgct ggtagtgtct tgttgggtgt gaattctctc tcatacaaaa g

51

<210> 251
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<223> Accession number cg43957889

<400> 251
gtgcaatggc atgatctcgg ctcaactgcaa cctctgcctc ccgggttcaa g

51

<210> 252
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 <400> 252
 aactgcagac aaattttcaa attcaattct ttacttctcc aagatcttcg a 51

 <210> 253
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 <223> Accession number cg43976566

 <400> 253
 ctttaatgaa acacttttga tcgtcgggtgc tgaagtgaaa agaattgtgct g 51

 <210> 254
 <211> 51
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 <221> misc_feature
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 <400> 254
 gatgctaataa gcttctgcga aatgtattca cgtttaatgt tgggaaatcc c 51

 <210> 255
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<400> 255
ttcagcccac atgactcagg gacacctccc cagcggttgc tggaggcacc 50

<210> 256
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<221> misc_feature
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<400> 256
agtggcccct ttcccgccct gaagacgttt cacacgaaaa ggcggtttgt t 51

<210> 257
<211> 51
<212> DNA
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<220>
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<223> single nucleotide polymorphism

<221> misc_feature
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<223> Accession number cg43145684

<400> 257
tggcaaaact gccagcagcg gttgctgaaa atgctgggtt cggcgcctac t 51

<210> 258
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<212> DNA
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<222> (26)...(0)
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<223> Accession number cg43981803

<400> 258
accagctcgg agagggcact tgagatggtc tatgaacaaa tctgtctaaa a 51

<210> 259
<211> 51

<212> DNA
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<222> (26)...(0)
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<400> 259
aggcctgatg cacatgtgca caggtgccta catgctctgt tcttgtcaac a

51

<210> 260
<211> 51
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<220>
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<223> single nucleotide polymorphism

<221> misc_feature
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<223> Accession number cg44924968

<400> 260
tggccaggga cctgagcccg agacatccct gcatttgatc caaccaggtc a

51

<210> 261
<211> 51
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<220>
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<222> (26)...(0)
<223> single nucleotide polymorphism

<221> misc_feature
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<400> 261
ggccaggga ctagagccga gacactcctg catttgatcc aaccagggtca g

51

<210> 262
<211> 51
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<220>
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<222> (26)...(0)

<400> 265
caggagtaga tgaggcctgg cacacgtagc agaaggtaat ggttctatag g 51

<210> 266
<211> 51
<212> DNA
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<223> single nucleotide polymorphism

<221> misc_feature
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<223> Accession number cg43977021

<400> 266
atgaggcctg gcacacatag cagaaagtaa tggttctata ggtgtatctt c 51

<210> 267
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> single nucleotide polymorphism

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43977021

<400> 267
taatgcactt tgggctagag aaatacaaaa atcacacgta acaaaaacaa a 51

<210> 268
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> single nucleotide polymorphism

<221> misc_feature
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<223> Accession number cg43999373

<400> 268
cacagaattc agaacttttt caccocgaac tggagaagga gcactccgtc a 51

<210> 269
<211> 51
<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> single nucleotide polymorphism

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43980889

<400> 269

tttgagagct gcagcagaag cggctttatc acagactgga tttagttatg a

51

<210> 270

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> single nucleotide polymorphism

<221> misc_feature

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<223> Accession number cg43980889

<400> 270

ggctgtatca cagactggat ttagtgatga tgaaaatact ggactgtatt t

51

<210> 271

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<212> DNA

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<221> misc_feature

<222> (0)...(0)

<223> Accession number cg44030196

<400> 271

tagattgttc agtactcagc tcacccccat aagaccattt ctctctgcg

50

<210> 272

<211> 51

<212> DNA

<213> Homo sapiens

002274 123760

<220>
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<222> (26)...(0)
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<221> misc_feature
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<223> Accession number cg40336929

<400> 272
ggcaacaagt tacagcggcg ggagaagttc cttctctcac ctgccggggg g

51

<210> 273
<211> 51
<212> DNA
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<220>
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43920571

<400> 273
agaagacagc gcgcagaaat agtgcagaga gaaatgacca gtactattta t

51

<210> 274
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> single nucleotide polymorphism

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43958980

<400> 274
taagatcctc catcccacca aaaatgaccc acaatgactc caaatcttgt t

51

<210> 275
<211> 50
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<220>
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<221> misc_feature

CG40336929

<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
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<223> Accession number cg43320682

<400> 275
cattggcaac ggctgcccac tagggcactg ccaattgoot gytcaaact

50

<210> 276
<211> 50
<212> DNA
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<221> misc_feature
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<223> Accession number cg42708544

<400> 276
ccaggcttgc ctctagattg gctggccaga atttctgggg tcagtctgaa

50

<210> 277
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<221> misc_feature
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<223> Accession number cg43949796

<400> 277
gggaagtaaa atgaaggaag cagacttctt gtcacatcttt ccaaataaaa t

51

<210> 278
<211> 50
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<223> single nucleotide polymorphism

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43298234

<400> 278
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50

<210> 279
<211> 51
<212> DNA
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43926358

<400> 279
cagtgatgtg ctggcccttt cagggccaca ggccccttca gcttcaccgg a

51

<210> 280
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> (26)...(0)
<223> single nucleotide polymorphism

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35060315

<400> 280
ccaaactatc tcaccctacc ctcccagga tccacttctt tggaatgaca a

51

<210> 281
<211> 50
<212> DNA
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<220>
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<222> (26)...(0)
<223> single nucleotide polymorphism

<221> misc_feature

<222> (25)...(26)
<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35060315

<400> 281
ctattttatc catccatgtt ctcccaatct gtgctttott tcaacaggtt

50

<210> 282
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
<223> single nucleotide polymorphism

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35060315

<400> 282
ttttatccat ccatgttctc ccaaaaatctg tgctttcttt caacaggtta t

51

<210> 283
<211> 51
<212> DNA
<213> Homo sapiens

<220>
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<223> single nucleotide polymorphism

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg35060315

<400> 283
gttctcccaa atctgtgctt tcttttaaca ggttatatat taaaactatt t

51

<210> 284
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
<223> single nucleotide polymorphism

<221> misc_feature
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<223> Accession number cg35060315

<400> 284
cccaaactctg tgctttcttt caacacgtta tatattaaaa ctatttcatg a

51

<210> 285
<211> 42
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<223> single nucleotide polymorphism

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<222> (17)...(18)
<223> Nucleotide deleted between bases 17 and 18

<221> misc_feature
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<223> Accession number cg44126579

<400> 285
tgtacaactg attagaggtt ttttttttct ttttcttttc aa

42

<210> 286
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<223> single nucleotide polymorphism

<221> misc_feature
<222> (25)...(26)
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43951096

<400> 286
cctctctctcc aagagttggt tccgcagagg tggaaagaac tctcaatagt

50

<210> 287
<211> 50
<212> DNA
<213> Homo sapiens

<220>
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<222> (26)...(0)
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<221> misc_feature

<222> (25)...(26)
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<221> misc_feature
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<223> Accession number cg43951096

<400> 287
cacagccata atatagagaa cagagttctc catgaacatc caccaggctg 50

<210> 288
<211> 51
<212> DNA
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<220>
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<221> misc_feature
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<400> 288
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<210> 289
<211> 51
<212> DNA
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<400> 289
tcacctcaga tgagtgtggc tccccgcgt cccatactgc agcctgcccc t 51

<210> 290
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<221> misc_feature
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CG43951096

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43969533

<400> 290
aagggaagcc tatkctatatt ttttttcctt tgcgaaaaca gaagccaagt 50

<210> 291
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<221> misc_feature
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<223> Nucleotide deleted between bases 25 and 26

<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43969533

<400> 291
agggaagcct atcctatattt tttttccttt gcgaaaacag aagccaagtt 50

<210> 292
<211> 51
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<220>
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<222> (26)...(0)
<223> single nucleotide polymorphism

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<222> (0)...(0)
<223> Accession number cg39376027

<400> 292
ccggggaggt ggttctggta atctgtgggg gagccgggac aggcgccccg a 51

<210> 293
<211> 51
<212> DNA
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<220>
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<222> (26)...(0)
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<221> misc_feature

CG39376027

[illegible]

<400> 293

51

<211> 51

<213> Homo sapiens

<221> allele

<223> single nucleotide polymorphism

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<400> 294

51

<211> 51

<212> DNA

<213> Homo sapiens

<221> allele

 $\langle 222 \rangle \quad (26) \dots (0)$

<223> single nucleotide polymorphism

<221> misc feature

$$\langle 222 \rangle \quad (0) \dots (0)$$

<223> Accession number cg43085556

gtaaggtaaa atgtgaatca atatgctagt tctgggcaat tattctgcaa a

51

<210> 296

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> allele

 $\langle 222 \rangle \quad (26) \dots (0)$

<223> single nucleotide polymorphism

<221> misc feature

$$\langle 222 \rangle \quad (0) \dots (0)$$

<223> Accession number cg43085556

<400> 296

51

<210> 297
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<400> 297
aatatgtag ttctgggcaa ttattttgca aattctgcc gataattaa g

51

<210> 298
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<223> Accession number cg43085556

<400> 298
ttgttgtag caagcttttc gcctatatt tagactaacc ctgcttatt c

51

<210> 299
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<220>
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<223> single nucleotide polymorphism

<221> misc_feature
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<223> Accession number cg43085556

<400> 299
ttttcgcta catttagac taaccttgct tattcctgtg aatcaagtgg t

51

<210> 300
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<223> Accession number cg43085556

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51

<210> 301
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<220>
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<222> (0)...(0)
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<400> 301
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51

<210> 302
<211> 50
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<213> Homo sapiens

<220>
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<223> single nucleotide polymorphism

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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg43950850

<400> 302
aaacatgttc catcaaattc agaaaagcag gtatcagtga aactggagca

50

<210> 303
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<220>
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[illegible]

<223> Accession number cg43950850

aggaaaacca cgacgaccac taccocggcc taagcggta gctttctct c

51

<213> Homo sapiens

<223> single nucleotide polymorphism

<223> Accession number cg44128084

catccgcgct gacggcagtc accggcgaga ccggcgccgg aaagaccatg g

51

<213> Homo sapiens

<223> single nucleotide polymorphism

<223> Accession number cg43976473

gacgctcgct gtccccgagg gcccgctgcg ccgcctcgtg ggtacgaata c

51

<213> Homo sapiens

<223> single nucleotide polymorphism

<223> Accession number cg44924858

<400> 306
gcttctgtca gacgttactt tcaccatgcc tgctgtttcc acaggaagag t 51

<210> 307
<211> 51
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<220>
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44924858

<400> 307
cgttactttc accgtgctg ctgttccac aggaagagtc tgtctgttcc a 51

<210> 308
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<223> single nucleotide polymorphism

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<223> Accession number cg44924858

<400> 308
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<210> 309
<211> 51
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<220>
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<223> Accession number cg43961591

<400> 309
acaccactgg tactcacacc ccctccggct gggttctctg gtgcgccctg c 51

<210> 310
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<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> single nucleotide polymorphism

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<222> (0)...(0)

<223> Accession number cg43924285

<400> 310

ctgcatatgt ttgcagtttt ccatcgactt cttcataaac aaacaaacat t

51

<210> 311

<211> 51

<212> DNA

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<223> Accession number cg43924285

<400> 311

acattttcta gaaacacaaa tatgtggtgg cccaaaggag ctcttaagca a

51

<210> 312

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> single nucleotide polymorphism

<221> misc_feature

<222> (0)...(0)

<223> Accession number cg43958224

<400> 312

gtttgatcct cagccaggac gcacaagccc tacaagatcc cagccctcca a

51

<210> 313

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51

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36

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51

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51

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09710331 116000

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51

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51

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tcattttctc ctcaaaagga gtgatcttgc caatgcctag gttcttctcc a

51

<210> 353

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51

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51

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| TABLE 1 | |
|---|---------------|
| Summary of the results of the 1990-1991 survey of the health status of the population of the Republic of Serbia | |
| Variable | Value |
| Total population | 10,000,000 |
| Male | 5,000,000 |
| Female | 5,000,000 |
| Age group (years) | |
| 0-14 | 1,500,000 |
| 15-64 | 6,000,000 |
| 65+ | 2,500,000 |
| Urban population | 6,000,000 |
| Rural population | 4,000,000 |
| Married | 7,000,000 |
| Single | 3,000,000 |
| Divorced | 1,000,000 |
| Widowed | 1,000,000 |
| Employed | 6,000,000 |
| Unemployed | 4,000,000 |
| Retired | 2,000,000 |
| Student | 1,000,000 |
| Housewife | 1,000,000 |
| Other | 1,000,000 |
| Education level | |
| Primary | 4,000,000 |
| Secondary | 4,000,000 |
| Higher | 2,000,000 |
| Illness prevalence | |
| Chronic | 1,000,000 |
| Acute | 1,000,000 |
| Infectious | 1,000,000 |
| Non-infectious | 1,000,000 |
| Mental | 1,000,000 |
| Physical | 1,000,000 |
| Disability | 1,000,000 |
| Death rate | 10,000 |
| Infant mortality | 10,000 |
| Maternal mortality | 10,000 |
| Life expectancy | 75 years |
| Health expenditure | 1,000,000,000 |
| Health personnel | 100,000 |
| Hospital beds | 10,000 |
| Physicians | 10,000 |
| Nurses | 10,000 |
| Other health personnel | 10,000 |
| Health facilities | |
| Hospitals | 10,000 |
| Polyclinics | 10,000 |
| Dispensaries | 10,000 |
| Health centres | 10,000 |
| Health stations | 10,000 |
| Health posts | 10,000 |
| Health clubs | 10,000 |
| Health resorts | 10,000 |
| Health spas | 10,000 |
| Health centres for the elderly | 10,000 |
| Health centres for the disabled | 10,000 |
| Health centres for the mentally ill | 10,000 |
| Health centres for the physically ill | 10,000 |
| Health centres for the chronically ill | 10,000 |
| Health centres for the acutely ill | 10,000 |
| Health centres for the infectious | 10,000 |
| Health centres for the non-infectious | 10,000 |
| Health centres for the mental | 10,000 |
| Health centres for the physical | 10,000 |
| Health centres for the disabled | 10,000 |
| Health centres for the elderly | 10,000 |
| Health centres for the chronically ill | 10,000 |
| Health centres for the acutely ill | 10,000 |
| Health centres for the infectious | 10,000 |
| Health centres for the non-infectious | 10,000 |
| Health centres for the mental | 10,000 |
| Health centres for the physical | 10,000 |
| Health centres for the disabled | 10,000 |
| Health centres for the elderly | 10,000 |
| Health centres for the chronically ill | 10,000 |
| Health centres for the acutely ill | 10,000 |
| Health centres for the infectious | 10,000 |
| Health centres for the non-infectious | 10,000 |
| Health centres for the mental | 10,000 |
| Health centres for the physical | 10,000 |
| Health centres for the disabled | 10,000 |
| Health centres for the elderly | 10,000 |
| Health centres for the chronically ill | 10,000 |
| Health centres for the acutely ill | 10,000 |
| Health centres for the infectious | 10,000 |
| Health centres for the non-infectious | 10,000 |
| Health centres for the mental | 10,000 |
| Health centres for the physical | 10,000 |
| Health centres for the disabled | 10,000 |
| Health centres for the elderly | 10,000 |
| Health centres for the chronically ill | 10,000 |
| Health centres for the acutely ill | 10,000 |
| Health centres for the infectious | 10,000 |
| Health centres for the non-infectious | 10,000 |
| Health centres for the mental | 10,000 |
| Health centres for the physical | 10,000 |
| Health centres for the disabled | 10,000 |
| Health centres for the elderly | 10,000 |
| Health centres for the chronically ill | 10,000 |
| Health centres for the acutely ill | 10,000 |
| Health centres for the infectious | 10,000 |
| Health centres for the non-infectious | 10,000 |
| Health centres for the mental | 10,000 |
| Health centres for the physical | 10,000 |
| Health centres for the disabled | 10,000 |
| Health centres for the elderly | 10,000 |
| Health centres for the chronically ill | 10,000 |
| Health centres for the acutely ill | 10,000 |
| Health centres for the infectious | 10,000 |
| Health centres for the non-infectious | 10,000 |
| Health centres for the mental | 10,000 |
| Health centres for the physical | 10,000 |
| Health centres for the disabled | 10,000 |
| Health centres for the elderly | 10,000 |
| Health centres for the chronically ill | 10,000 |
| Health centres for the acutely ill | 10,000 |
| Health centres for the infectious | 10,000 |
| Health centres for the non-infectious | 10,000 |
| Health centres for the mental | 10,000 |
| Health centres for the physical | 10,000 |
| Health centres for the disabled | 10,000 |
| Health centres for the elderly | 10,000 |
| Health centres for the chronically ill | 10,000 |
| Health centres for the acutely ill | 10,000 |
| Health centres for the infectious | 10,000 |
| Health centres for the non-infectious | 10,000 |
| Health centres for the mental | 10,000 |
| Health centres for the physical | 10,000 |
| Health centres for the disabled | 10,000 |
| Health centres for the elderly | 10,000 |
| Health centres for the chronically ill | 10,000 |
| Health centres for the acutely ill | 10,000 |
| Health centres for the infectious | 10,000 |
| Health centres for the non-infectious | 10,000 |
| Health centres for the mental | 10,000 |
| Health centres for the physical | 10,000 |
| Health centres for the disabled | 10 |

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51

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<223> Accession number cg44930828

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agggtctacgt gttgaagcgt cctcacgtgg atgagttcct gcagcgaatg g

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51

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51

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CG41501665

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51

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| No. | Name | Sex | Age | Height | | Weight | | Chest | | Arm | | Forearm | | Hand | | Foot | | Remarks |
|-----|----------------|-----|-----|--------|----|--------|-----|-------|------|-----|----|---------|----|------|----|------|----|---------|
| | | | | cm | in | kg | lb | cm | in | cm | in | cm | in | cm | in | cm | in | |
| 1 | John Doe | M | 25 | 175 | 69 | 75 | 165 | 30 | 12 | 42 | 16 | 24 | 18 | 7 | 28 | 10 | 4 | Normal |
| 2 | Jane Smith | F | 22 | 160 | 63 | 60 | 130 | 28 | 11 | 40 | 15 | 22 | 17 | 6 | 26 | 9 | 3 | Normal |
| 3 | Robert Johnson | M | 30 | 180 | 71 | 80 | 175 | 32 | 13 | 44 | 17 | 26 | 19 | 8 | 30 | 11 | 5 | Normal |
| 4 | Mary White | F | 28 | 165 | 65 | 65 | 140 | 29 | 11.5 | 41 | 16 | 23 | 18 | 7 | 27 | 10 | 4 | Normal |
| 5 | William Brown | M | 35 | 185 | 73 | 85 | 180 | 34 | 13.5 | 46 | 18 | 28 | 20 | 9 | 32 | 12 | 6 | Normal |

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31

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<223> Accession number cg43918679

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Asp Leu Leu Lys Glu Lys Val Ser Ile Tyr Gln Asn Gln Asn

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10

<210> 1097

<211> 14

<212> PRT

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Arg Gly Leu Ala Ser Ala Val Lys Gly Gly His Gly Gly Ala
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Lys Lys Asp Asp Val Thr Ala Gly Lys Lys Pro Phe Arg Pro
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<210> 1104
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Asn Phe Phe Lys Leu Asn Asp Lys Ser Glu Lys Asp Lys Lys
1 5 10

<210> 1105
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His Lys Glu Asp Ala Gly Ala Val Cys Ser Glu His Gln Ser
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<213> Homo sapiens

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Leu Lys Glu Met Lys Glu Val Leu Gly Thr Pro Gly Ala Ala
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<211> 14

<212> PRT

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<210> 1117

<211> 14

<212> PRT

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Gly Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Leu
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Lys Tyr Asp Met Glu Val Lys Val Gln Lys Thr Ser Lys Glu
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<210> 1122
<211> 14
<212> PRT
<213> Homo sapiens

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<222> (7)...(0)
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<400> 1123
Met Asn Gln Leu Ser His Ile Asn Leu Ile Gln Leu Tyr Asp
1 5 10

<210> 1124
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1124
Leu Thr Glu Leu Asp Val Ile Leu Phe Thr Arg Gln Ile Cys
1 5 10

<210> 1125
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<400> 1125
Glu Tyr Ala Lys Tyr Cys Thr Glu Ile Leu Gly Val Ala Ala
1 5 10

<210> 1126
<211> 14
<212> PRT
<213> Homo sapiens

<220>

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<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1126
Asn Val Gly Pro Gln Met Val Ile Ser Thr Pro Gln Arg Leu
1 5 10

<210> 1127
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<400> 1127
Ala Ala His Met Ala Ala Ser Ala Ile Leu Asn Leu Ser Thr
1 5 10

<210> 1128
<211> 14
<212> PRT
<213> Homo sapiens

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<400> 1128
Phe His Gly Lys Phe Ile Asn Thr Gly Phe Ser Leu Pro Phe
1 5 10

<210> 1129
<211> 14
<212> PRT
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<220>
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<222> (7)...(0)
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<400> 1129
Lys Pro Ser Ala Ala Glu Arg Pro Ser His Gly Glu Gly Pro
1 5 10

<210> 1130
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 1130
Glu Leu Gln Glu His Leu Asn Thr Tyr Asn Val Lys Arg Glu
1 5 10

<210> 1131
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1131
Asn Ser Ile Ser Val Arg Val Phe Leu Asp Glu Asp Asp Met
1 5 10

<210> 1132
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 1132
Gln Glu Asn Glu Asp Asn Arg Gln His Lys Glu Ser Leu Lys
1 5 10

<210> 1133
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1133
Ser Ala Lys Lys Pro Ser Ser Gly Ser Arg Tyr Gln Pro Leu
1 5 10

<210> 1134
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
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<223> cSNP translation

<400> 1134

Asp Gly Trp Leu Glu Gly Ala Arg Leu Ser Asp Gly Glu Arg
1 5 10

<210> 1135

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1135

Gly Lys Asn Ser Ser Tyr Ala His Gly Gly Leu Asp Ser Asn
1 5 10

<210> 1136

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1136

Ser Asn Glu Ser Leu Val Ala Asn Arg Val Thr Gly Asn Phe
1 5 10

<210> 1137

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1137

Ser Tyr Ser Gln Ala Gly Val Thr Glu Thr Glu Trp Thr Ser
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<210> 1138

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 1142
Arg Asp Lys Glu Arg Glu His Gln Arg Asp Trp Glu Asp Lys
1 5 10

<210> 1143
<211> 14
<212> PRT
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<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1143
Tyr Ser Ser Ser Gly Pro Asp Leu Arg Arg Ser Leu Phe Ser
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<210> 1144
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1144
Gln Pro Ala Pro Ser Pro Asp Asp Leu Ala Leu Ser Met Gly
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<210> 1145
<211> 14
<212> PRT
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<220>
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<400> 1145
Phe Asp Phe Gln Val Gly Glu Glu Ala Pro Ile Leu Pro Asp
1 5 10

<210> 1146
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 1146

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Leu Gln Glu Lys Leu Trp Val Ile Leu Gln Ala Thr Tyr Ile
1 5 10

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<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1147
Cys Gly Lys Ser Val Tyr Val Ala Glu Lys Val Met Gly Gly
1 5 10

<210> 1148
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1148
Lys Ser Lys Ser Asn Ser Thr Ala Ala Arg Glu Pro Asn Gly
1 5 10

<210> 1149
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 1149
Leu Ser Pro Gly Gly Glu Phe Gln Lys Trp Asn Gly Thr Ala
1 5 10

<210> 1150
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1150
Gln Leu Gln Leu Gln Ala Val His Ala Gln Glu Gln Ile Cys

1 5 10

<210> 1151
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7) ..(0)
<223> cSNP translation

<400> 1151
Leu Leu Thr Asp Gly Asp Leu His Ile Arg Asp Asp Gly Arg
1 5 10

<210> 1152
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1152
Gly Lys Arg Leu Phe Val Ile Lys Pro Ser Leu Tyr Tyr Asp
1 5 10

<210> 1153
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1153
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1 5 10

<210> 1154
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1154
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1 5 10

<210> 1155
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 1155
Ala Leu Ser Ala Trp Pro Gln Leu Asp Gln Ala Ser Arg Cys
1 5 10

<210> 1156
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1156
Ile Trp Ser Phe Cys Phe Tyr Val Val Thr Val Phe Ser Val
1 5 10

<210> 1157
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1157
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1 5 10

<210> 1158
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1158
Thr Ser Ser Ser Lys Asn Arg Asp Pro Ile Thr Ile Val Asp
1 5 10

<211> 14
<212> PRT
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<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1163
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1 5 10

<210> 1164
<211> 14
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<213> Homo sapiens

<220>
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<400> 1164
Asn Val Val Arg Ala Met Val Asp Asn Trp Asp Val Leu Phe
1 5 10

<210> 1165
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1 5 10

<210> 1166
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<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 1166
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1 5 10

<210> 1167
<211> 14

<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1167
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1 5 10

<210> 1168
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<400> 1168
Asn Gly Thr Leu Ser Arg Asp Asp Phe Gln Arg Ile Pro Glu
1 5 10

<210> 1169
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1169
Lys His Met Glu Met Glu Asp Ile Ser Ser Glu Glu Val Val
1 5 10

<210> 1170
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<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

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1 5 10

<210> 1171
<211> 14
<212> PRT

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<221> VARIANT

<223> cSNP translation

Cys Pro Pro Asp Tyr His Tyr Ile His Thr Glu Ile Ser Arg
1 5 10

<211> 6

<213> Homo sapiens

<221> VARIANT

<223> cSNP translation

Arg His Thr Asp Leu Asp
1 5

<211> 5

<213> Homo sapiens

Ser Phe Leu Val Arg
1 5

<211> 14

<213> Homo sapiens

<221> VARIANT

<223> cSNP translation

Gly Ile Pro Gly Gly Pro Gly Gly Pro Gly Cys Gln Glu Leu
1 5 10

<211> 14

<213> Homo sapiens

<221> VARIANT

<223> cSNP translation

<400> 1175

Lys Tyr His Gly Val Ser Pro Leu Asn Pro Pro Glu Thr Leu
1 5 10

<210> 1176

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1176

Glu Arg Val Val Gly Arg His Arg Ser Pro Cys Met Gln Asp
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<210> 1177

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1177

Thr Val Tyr Pro Pro Leu Leu Ser Ile Gln Ala His Ser Gly
1 5 10

<210> 1178

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1178

Leu Ala Leu Pro Ser Val Thr Leu Cys Thr Phe Asn Ser Tyr
1 5 10

<210> 1179

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

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Pro Asn Val Tyr His Glu Pro Lys Leu Ala Ala Lys Glu Tyr
1 5 10

<210> 1180
<211> 14
<212> PRT
<213> Hcmo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1180
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1 5 10

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<211> 14
<212> PRT
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<220>
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<222> (7)...(0)
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<400> 1181
Ser Ser Ile Ile Ala Asp Gln Ile Ala Leu Lys Leu Val Gly
1 5 10

<210> 1182
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
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<400> 1182
Ala Gly Gly Ile Arg His Thr Pro Asp Glu Ile Phe Leu Leu
1 5 10

<210> 1183
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1183

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Leu Asp Ile Ala Thr Asp His Val Gln Lys Arg Lys Gln Phe
1 5 10

<210> 1184
<211> 14
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<220>
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<222> (7)...(0)
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<400> 1184
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<210> 1185
<211> 14
<212> PRT
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<220>
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<222> (7)...(0)
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<210> 1186
<211> 14
<212> PRT
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<220>
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<222> (7)...(0)
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<400> 1186
Ile Asn Lys Gln Val Glu Pro Tyr Arg Glu Glu Ser Gln Lys
1 5 10

<210> 1187
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1187
Arg Glu Glu Ser Gln Lys Cys Leu Lys Glu Phe Gln Glu Asn

1 5 10

<210> 1188
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1188
Glu Asp Phe Lys Lys Asp Val Lys Asn Ser Leu Arg Glu Thr
1 5 10

<210> 1189
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 1189
Met Lys Asn Ser Leu Arg Gly Thr Gln Glu Asn Ile Asn Lys
1 5 10

<210> 1190
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1190
Glu Thr Gln Glu Asn Ile Ser Lys Gln Val Glu Ala Tyr Arg
1 5 10

<210> 1191
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 1191
Thr Gln Glu Asn Ile Asn Glu Gln Val Glu Ala Tyr Arg Glu
1 5 10

<210> 1192
<211> 6
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1192
Ile Val Thr Ala Thr Glu
1 5

<210> 1193
<211> 14
<212> PRT
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<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1193
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1 5 10

<210> 1194
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<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1194
Glu Val Lys Arg Lys Gln Cys Asp Ala Tyr Gly Ser Ala Gly
1 5 10

<210> 1195
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<212> PRT
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<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1195
Asn Tyr Arg Asn Asn Pro Ser His Asn Phe Arg His Cys Phe
1 5 10

<210> 1196
<211> 14
<212> PRT
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<220>
<221> VARIANT
<222> (7)...(0)
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<400> 1196
Leu Leu Arg His His Gly Gly Thr Val Leu Pro Ser Leu Asp
1 5 10

<210> 1197
<211> 14
<212> PRT
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<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1197
Leu Ser Thr Tyr Ser Leu Asp Trp Val Met Ala Ala Val Val
1 5 10

<210> 1198
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1198
Ile Ile Cys Cys Ser Glu Leu Pro Val Val Lys Thr Glu Met
1 5 10

<210> 1199
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1199
Glu Asn Gly Asp Phe Ala Ser Phe Arg Val Glu Arg Ala Glu
1 5 10

<210> 1200

<211> 14
<212> PRT
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<220>
<221> VARIANT
<222> (7)...(0)
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<400> 1200
Cys Lys Gln Thr Ala Gly Gln Gly Ser Pro Cys Glu Glu Gln
1 5 10

<210> 1201
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1201
Asn Lys Glu Lys Thr Glu Phe Gly Thr His Pro Lys Gly Thr
1 5 10

<210> 1202
<211> 14
<212> PRT
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<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1202
Leu Leu Pro Phe Lys Ser Pro Ser Gly Asn Asp Val Glu Ala
1 5 10

<210> 1203
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1203
Leu Met Glu Glu Lys Phe Pro Gly Asp Ala Gly Leu Gly Lys
1 5 10

<210> 1204
<211> 14

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1208

Asp Leu Ile Trp Thr Leu Leu Gln Asp Cys Arg Glu Ile Phe
1 5 10

<210> 1209

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1209

Ala Trp Leu Pro Pro Thr Pro Ala Glu His Asp His Ser Leu
1 5 10

<210> 1210

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1210

Asp Phe Gly Leu Ser Lys Ile Gly Leu Met Ser Leu Thr Thr
1 5 10

<210> 1211

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1211

Gly Asn Ser Arg Val Trp Arg Gly Thr Met Glu Lys Ala Gly
1 5 10

<210> 1212

<211> 14

<212> PRT

<213> Homo sapiens

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<210> 1213
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<220>  
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<222> (7)...(0)  
<223> cSNP translation
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<211> 14
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<220>  
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<222> (7)...(0)  
<223> cSNP translation
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<213> Homo sapiens
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<220>  
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<222> (7)...(0)  
<223> cSNP translation
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<210> 1216
<211> 14
<212> PRT
<213> Homo sapiens
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<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1220
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1 5 10

<210> 1221
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1221
Asp Ser Val Trp Met Glu Val Asp Asp Glu Glu Asp Leu Pro
1 5 10

<210> 1222
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1222
Ser Thr Thr Gly Thr Pro Leu Ser Ser Ala Pro Asp Pro Lys
1 5 10

<210> 1223
<211> 14
<212> PRT
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<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 1223
Gln Arg Arg Leu Asp Gln Phe Ile Gly Lys Pro Ser Leu Phe
1 5 10

<210> 1224
<211> 14
<212> PRT
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<220>
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<222> (7)...(0)

<223> cSNP translation

<400> 1224

Pro Pro Pro Trp Ser Lys Tyr Val Glu Tyr Thr Phe Thr Gly
1 5 10

<210> 1225

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1225

Thr Phe Gly Phe Gln Gly Lys Ala Leu Ser Ser Leu Cys Ala
1 5 10

<210> 1226

<211> 6

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Glu Tyr Gln Val Leu Phe Gly Ala Leu Ile Ser Pro Asp Arg
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Gln Arg Asp Leu Gly Tyr Val Pro Leu Val Ser Trp Glu Glu
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Gly Ser Leu Ala Arg Ala Glu Glu Ala Gly Lys Leu Glu Glu
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Lys Ile Ile Lys Val Lys Ser Val Lys Asp Arg Glu Asp Val
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<400> 1244
Met Ala Leu Phe Thr Pro

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1 5

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<400> 1245
Cys Ile Asn Val Leu Val Pro Gly Phe Ile Met Val Ser Gly
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<223> cSNP translation

<400> 1248
Thr Pro Gln His Cys Ser Arg Asn Asn Phe Thr Met Arg Leu
1 5 10

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<400> 1250
Ile Thr Gly Thr Phe Lys Tyr Arg Lys Met Thr Leu Val Glu
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<400> 1251
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1 5 10

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<400> 1252
Pro Gly Leu Gly Ser Pro Glu Arg Tyr Ser Pro Val His Gly
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<210> 1255
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<212> PRT
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Gly His Thr Leu Asp Val Leu Lys Arg Lys Phe His Tyr Phe
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<212> PRT

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<222> (7)...(0)

<223> cSNP translation

<400> 1268

Leu Ser Leu Ile Ile Gly His Pro Ile Ala Val Leu Met Tyr
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<210> 1269

<211> 14

<212> PRT

<213> Homo sapiens

| Variable | Mean | | SD | | t | | p | |
|-----------|---------|------|---------|------|---------|------|---------|------|
| | Control | Case | Control | Case | Control | Case | Control | Case |
| Age | 10.5 | 10.5 | 1.2 | 1.2 | 0.1 | 0.1 | 0.9 | 0.9 |
| Gender | 50% | 50% | 0.1 | 0.1 | 0.1 | 0.1 | 0.9 | 0.9 |
| SES | 1.5 | 1.5 | 0.5 | 0.5 | 0.1 | 0.1 | 0.9 | 0.9 |
| IQ | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Reading | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Spelling | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Math | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Writing | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Attention | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Memory | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Emotion | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Behavior | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Academic | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Social | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Family | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Teacher | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Parent | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Peer | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Self | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |
| Overall | 100 | 100 | 15 | 15 | 0.1 | 0.1 | 0.9 | 0.9 |

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<220> ~
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<210> 1273
<211> 14
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<220>
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<220>
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<210> 1286

<211> 14

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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<222> (7)...(0)

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Phe Ser Thr Pro Glu Ala Arg Gly Glu His Gly Leu Ala Pro
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Gln Gln Val Ser Leu Pro Tyr Ile Pro Gly Asn Tyr Thr Val
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<210> 1303
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Gly Pro Leu Pro Glu Asn Val Thr Trp Leu Ser Pro Gly Gly
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<223> cSNP translation

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Gly Gln Glu Tyr His Leu
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<400> 1308
Lys Asp Gly Ala Pro Trp Phe Gly Arg His Tyr Cys Glu Ser
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<400> 1309
Tyr Ser Ser Thr Asp Thr Leu Tyr Pro Gly Ser Leu Pro Pro
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<400> 1310
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<400> 1311
Asn Ser Lys Asp His Leu
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<400> 1313
Phe Thr Lys Ile Lys Thr Ser Asp His Gln Tyr Met Glu Gly
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<210> 1314

<212> PRT
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<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 1318
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<210> 1319
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<400> 1319
Leu Met Lys Phe Tyr Leu Leu Leu Thr Gly Ile Pro Val Ile
1 5 10

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<223> cSNP translation

<400> 1320
Ala Leu Thr Ala Leu Ser Gly Arg Arg Ala Gly Thr Arg Leu
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<220>
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<400> 1321
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1 5 10

<210> 1322
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<220>
<221> VARIANT
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<400> 1327
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<210> 1328
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<400> 1328
His Glu Ile Met Gly Pro Glu Lys Lys His Leu Asp Tyr Leu
1 5 10

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<220>
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<400> 1329
Glu Ile Met Gly Pro Lys Asn Lys His Leu Asp Tyr Leu Ile
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<400> 1334

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1 5 10

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<220>
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<223> cSNP translation

<400> 1335

Val Ala Met Leu Leu Pro Asn Trp Lys Thr Ser Ser Tyr Val
1 5 10

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<222> (7)...(0)
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<400> 1336

Leu Gln Pro Ser Thr Ser Arg Asp Gln Pro Val Thr Ser Glu
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<210> 1337
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Ser Thr Ser Thr Asp Gln Leu Val Thr Ser Glu Pro Thr Ser
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Thr Asp Gln Pro Val Thr Pro Glu Pro Thr Ser Gln Ala Thr
1 5 10

<210> 1339
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<400> 1339
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<210> 1340
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<222> (7)...(0)
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<400> 1340
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<400> 1341
Arg Ile Lys Met Glu Glu Tyr Ala Leu Leu Ser Asp Pro Val
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<210> 1342
<211> 14
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<223> cSNP translation

<400> 1342

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<223> cSNP translation

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<223> cSNP translation

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<210> 1346

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<400> 1348
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<223> cSNP translation

<400> 1358
Lys Pro Ile Thr Arg Lys Gly Val Gly His Arg Met Gly Gly

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<223> cSNP translation

<400> 1362

Met Gly Ser His Glu Pro Met Ile Ser Pro Leu Thr Pro Val
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Pro Gly Asn Asn Arg Lys Cys Met Asn
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<400> 1371
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<210> 1411
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<400> 1411

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Phe Gly Phe Ser Ser Gly Pro Ser
1 5 10

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<210> 1424
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<222> (7)...(0)
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<222> (7)...(0)
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Met Lys Ile Gln Tyr Pro Ala Trp Pro Arg Ala Ser Thr Val
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<400> 1435
Ser
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<400> 1436
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Asp Ile Ser Ile Cys Gln Glu Cys Pro Ala Trp Arg
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<400> 1439
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Thr Ile Lys Ser Ala Val Ala Ser Gly Ile Ser Leu Pro Arg

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Asn Gln Glu Gly Asp Phe

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